GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 12:45:07 ; Search time 2035 Seconds
(without alignments)
6316.183 Million cell updates/sec

Title: US-10-796-280-19350
Perfect score: 200.6
Sequence: 1 ttgacatcctcatcttttct.....tcttcaccccacgctggtga 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	200.6	100.0	135751	5	AL596089	AL596089 Human DNA
c 2	200.6	100.0	194321	12	AC027197	AC027197 Homo sapi
3	187.8	93.6	331	5	HUMPLG20	M34272 Human plasm
4	187.8	93.6	55266	5	AY192161	AY192161 Homo sapi
5	186.2	92.8	163599	5	HSDJ81D8	AL109933 Human DNA
c 6	186.2	92.8	177878	12	AC010893	AC010893 Homo sapi
c 7	174	86.7	179154	12	AC084862	AC084862 Papio anu
c 8	156.2	77.9	171010	12	AC084863	AC084863 Papio anu
9	154.6	77.1	194321	12	AC027197	AC027197 Homo sapi
10	144.4	72.0	13869	2	DD181590	DD181590 LIPID-ASS
11	144.4	72.0	13938	5	HSALIPOA	X06290 Human mRNA
c 12	144.2	71.9	150377	12	AC093405	AC093405 Lemur cat
13	132.6	66.1	744	2	AX815991	AX815991 Sequence
14	132.6	66.1	750	2	AX463624	AX463624 Sequence
15	132.6	66.1	750	2	AX815990	AX815990 Sequence
16	132.6	66.1	783	2	AX815989	AX815989 Sequence
17	132.6	66.1	786	2	AX815988	AX815988 Sequence
18	132.6	66.1	999	2	AX815985	AX815985 Sequence
19	132.6	66.1	1005	2	AX815983	AX815983 Sequence
20	132.6	66.1	1011	2	AX815986	AX815986 Sequence
21	132.6	66.1	1017	2	AX815984	AX815984 Sequence
22	132.6	66.1	1038	2	AX815981	AX815981 Sequence
23	132.6	66.1	1041	2	AX815979	AX815979 Sequence
24	132.6	66.1	1047	2	AX463626	AX463626 Sequence
25	132.6	66.1	1047	2	AX815987	AX815987 Sequence
26	132.6	66.1	1050	2	AX815982	AX815982 Sequence
27	132.6	66.1	1053	2	AX815980	AX815980 Sequence
28	132.6	66.1	1302	2	AX815977	AX815977 Sequence
29	132.6	66.1	1314	2	AX815978	AX815978 Sequence
30	132.6	66.1	1724	2	AR363268	AR363268 Sequence
31	132.6	66.1	1784	5	HUMPMGM	K02922 Human plasm
32	132.6	66.1	1907	2	AR583729	AR583729 Sequence
33	132.6	66.1	1907	2	AX616369	AX616369 Sequence
34	132.6	66.1	2145	2	AX815993	AX815993 Sequence
35	132.6	66.1	2296	2	AR105749	AR105749 Sequence
36	132.6	66.1	2296	2	I14104	I14104 Sequence 18
37	132.6	66.1	2376	2	AX815992	AX815992 Sequence
38	132.6	66.1	2400	2	AX815934	AX815934 Sequence
39	132.6	66.1	2412	2	AX815936	AX815936 Sequence
40	132.6	66.1	2430	2	AR243324	AR243324 Sequence
41	132.6	66.1	2432	2	CS200978	CS200978 Sequence
42	132.6	66.1	2433	2	AX463622	AX463622 Sequence
43	132.6	66.1	2433	2	AX815938	AX815938 Sequence
44	132.6	66.1	2497	2	AR037325	AR037325 Sequence
45	132.6	66.1	2497	2	AR082437	AR082437 Sequence

ALIGNMENTS

RESULT 1
AL596089/c
LOCUS AL596089 135751 bp DNA linear PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP11-414A5 on chromosome 6 Contains the 3' end of the LPA gene for lipoprotein (Lp(a)) and a CpG island, complete sequence.
ACCESSION AL596089
VERSION AL596089.19 GI:21425227
KEYWORDS HTG; apolipoprotein; CpG island; kringle; lipoprotein; LPA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 135751)
AUTHORS Sycamore,N.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
COMMENT On Jun 13, 2002 this sequence version replaced gi:21261809.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-414A5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
---------- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

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FEATURES             Location/Qualifiers
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Qy        181 GTCTTCACCCCACGCTGGTGA 201
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RESULT 2
AC027197/c
LOCUS       AC027197               194321 bp    DNA     linear   HTG 24-AUG-2002
DEFINITION  Homo sapiens chromosome 6 clone RP11-189O14 map 6, LOW-PASS
            SEQUENCE SAMPLING.
ACCESSION   AC027197
VERSION     AC027197.3  GI:9887745
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 194321)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 6, clone RP11-189O14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 194321)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 194321)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Aug 24, 2000 this sequence version replaced gi:9799792.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L7625
                Center clone name: 189_O_14
            --------------.
            * NOTE: This record contains 224 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      741: contig of 741 bp in length
            *      742      841: gap of 100 bp
            *      842     1594: contig of 753 bp in length
            *     1595     1694: gap of 100 bp
            *     1695     2442: contig of 748 bp in length
            *     2443     2542: gap of 100 bp
            *     2543     3274: contig of 732 bp in length
            *     3275     3374: gap of 100 bp
            *     3375     4104: contig of 730 bp in length
            *     4105     4204: gap of 100 bp
            *     4205     4929: contig of 725 bp in length
            *     4930     5029: gap of 100 bp
            *     5030     5737: contig of 708 bp in length
            *     5738     5837: gap of 100 bp
            *     5838     6574: contig of 737 bp in length
            *     6575     6674: gap of 100 bp
            *     6675     7382: contig of 708 bp in length
            *     7383     7482: gap of 100 bp
            *     7483     8227: contig of 745 bp in length
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*     8228     8327: gap of 100 bp
*     8328     9072: contig of 745 bp in length
*     9073     9172: gap of 100 bp
*     9173     9920: contig of 748 bp in length
*     9921    10020: gap of 100 bp
*    10021    10740: contig of 720 bp in length
*    10741    10840: gap of 100 bp
*    10841    11566: contig of 726 bp in length
*    11567    11666: gap of 100 bp
*    11667    12407: contig of 741 bp in length
*    12408    12507: gap of 100 bp
*    12508    13254: contig of 747 bp in length
*    13255    13354: gap of 100 bp
*    13355    14095: contig of 741 bp in length
*    14096    14195: gap of 100 bp
*    14196    14933: contig of 738 bp in length
*    14934    15033: gap of 100 bp
*    15034    15755: contig of 722 bp in length
*    15756    15855: gap of 100 bp
*    15856    16584: contig of 729 bp in length
*    16585    16684: gap of 100 bp
*    16685    17433: contig of 749 bp in length
*    17434    17533: gap of 100 bp
*    17534    18286: contig of 753 bp in length
*    18287    18386: gap of 100 bp
*    18387    19127: contig of 741 bp in length
*    19128    19227: gap of 100 bp
*    19228    19937: contig of 710 bp in length
*    19938    20037: gap of 100 bp
*    20038    20750: contig of 713 bp in length
*    20751    20850: gap of 100 bp
*    20851    21574: contig of 724 bp in length
*    21575    21674: gap of 100 bp
*    21675    22395: contig of 721 bp in length
*    22396    22495: gap of 100 bp
*    22496    23225: contig of 730 bp in length
*    23226    23325: gap of 100 bp
*    23326    24072: contig of 747 bp in length
*    24073    24172: gap of 100 bp
*    24173    24902: contig of 730 bp in length
*    24903    25002: gap of 100 bp
*    25003    25746: contig of 744 bp in length
*    25747    25846: gap of 100 bp
*    25847    26585: contig of 739 bp in length
*    26586    26685: gap of 100 bp
*    26686    27376: contig of 691 bp in length
*    27377    27476: gap of 100 bp
*    27477    28217: contig of 741 bp in length
*    28218    28317: gap of 100 bp
*    28318    29039: contig of 722 bp in length
*    29040    29139: gap of 100 bp
*    29140    29876: contig of 737 bp in length
*    29877    29976: gap of 100 bp
*    29977    30717: contig of 741 bp in length
*    30718    30817: gap of 100 bp
*    30818    31554: contig of 737 bp in length
*    31555    31654: gap of 100 bp
*    31655    32380: contig of 726 bp in length
*    32381    32480: gap of 100 bp
*    32481    33227: contig of 747 bp in length
*    33228    33327: gap of 100 bp
*    33328    34072: contig of 745 bp in length
*    34073    34172: gap of 100 bp
*    34173    34896: contig of 724 bp in length
*    34897    34996: gap of 100 bp
*    34997    35739: contig of 743 bp in length
*    35740    35839: gap of 100 bp
*    35840    36559: contig of 720 bp in length
*    36560    36659: gap of 100 bp
*    36660    37395: contig of 736 bp in length
*    37396    37495: gap of 100 bp
*    37496    38105: contig of 610 bp in length
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*    38206    38948: contig of 743 bp in length
*    38949    39048: gap of 100 bp
*    39049    39799: contig of 751 bp in length
*    39800    39899: gap of 100 bp
*    39900    40646: contig of 747 bp in length
*    40647    40746: gap of 100 bp
*    40747    41467: contig of 721 bp in length
*    41468    41567: gap of 100 bp
*    41568    42307: contig of 740 bp in length
*    42308    42407: gap of 100 bp
*    42408    43130: contig of 723 bp in length
*    43131    43230: gap of 100 bp
*    43231    43963: contig of 733 bp in length
*    43964    44063: gap of 100 bp
*    44064    44771: contig of 708 bp in length
*    44772    44871: gap of 100 bp
*    44872    45584: contig of 713 bp in length
*    45585    45684: gap of 100 bp
*    45685    46436: contig of 752 bp in length
*    46437    46536: gap of 100 bp

  Query Match             100.0%;  Score 200.6;  DB 12;  Length 194321;
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Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Db      10570 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 10511

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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Db      10510 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 10451

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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Db      10450 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 10391

Qy        181 GTCTTCACCCCACGCTGGTGA 201
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Db      10390 GTCTTCACCCCACGCTGGTGA 10370


RESULT 3
HUMPLG20
LOCUS       HUMPLG20                  331 bp    DNA     linear   PRI 07-JAN-1995
DEFINITION  Human plasminogen gene, exon 16.
ACCESSION   M34272 J05286
VERSION     M34272.1  GI:190060
KEYWORDS    plasminogen.
SEGMENT     20 of 24
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 331)
  AUTHORS   Petersen,T.E., Martzen,M.R., Ichinose,A. and Davie,E.W.
  TITLE     Characterization of the gene for human plasminogen, a key proenzyme
            in the fibrinolytic system
  JOURNAL   J. Biol. Chem. 265 (11), 6104-6111 (1990)
   PUBMED   2318848
COMMENT     Original source text: Homo sapiens DNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by A.Ichinose, 26-MAR-1990, for release after publication.
FEATURES             Location/Qualifiers
     source          1. .331
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="6q26-q27"
                     /cell_type="leukocyte and lung fibroblast"
     intron          <1. .40
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                     /number=16
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                     /number=16
ORIGIN      Undetermined number of base pairs after segment 19.

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  Best Local Similarity   95.5%;  Pred. No. 4.6e-47;
  Matches  192;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | ||||||||||||||:||||||||||||||||||
Db         79 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 138

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  ||||||||||||||||||||||||||||||||| |||||||||
Db        139 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 198

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db        199 GTCTTCACCCCACGCTGGTGA 219


RESULT 4
AY192161
LOCUS       AY192161               55266 bp    DNA     linear   PRI 18-DEC-2002
DEFINITION  Homo sapiens plasminogen (PLG) gene, complete cds.
ACCESSION   AY192161
VERSION     AY192161.1  GI:27228744
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 55266)
  AUTHORS   Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A.,
            Rajkumar,N., Toth,E.J., Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-DEC-2002) Genome Sciences, University of Washington,
            1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI HL66682 Program
            for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.gs.washington.edu).
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                     /db_xref="taxon:9606"
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     variation       406
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                     GPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAHG
                     YIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCL
                     KGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPW
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                     LKKCSGTEASVVAPPPVVLLPDVETPSEEDCMFGNGKGYRGKRATTVTGTPCQDWAAQ
                     EPHRHSIFTPETNPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLYDYCDVPQCAAPSFD
                     CGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCL
                     EKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTRKDIALLKLSSPAVITDKVI
                     PACLPSPNYVVADRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQ
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  Matches  192;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Db      39282 TTGACATCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 39341

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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Db      39342 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 39401

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  ||||||||||||||||||||||||||||||||| |||||||||
Db      39402 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 39461

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      39462 GTCTTCACCCCACGCTGGTGA 39482


RESULT 5
HSDJ81D8
LOCUS       HSDJ81D8               163599 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP1-81D8 on chromosome 6q25.3-26
            Contains the PLG gene for plasminogen, the 5' end of the LPA gene
            for lipoprotein (Lp(a)), a novel gene, a pseudogene similar to part
            of plasminogen and a CpG island, complete sequence.
ACCESSION   AL109933
VERSION     AL109933.25  GI:11344445
KEYWORDS    HTG; apolipoprotein; CpG; kringle; lipoprotein; LPA; plasminogen;
            PLG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 163599)
  AUTHORS   Tracey,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 25, 2000 this sequence version replaced gi:11322966.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr6
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
```

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          Web site: http://www.sanger.ac.uk
          Contact: vega@sanger.ac.uk
          --------------
          This sequence was finished as follows unless otherwise noted: all
          regions were either double-stranded or sequenced with an alternate
          chemistry or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by at least
          one subclone; and the assembly was confirmed by restriction digest,
          except on the rare occasion of the clone being a YAC.
          RP1-81D8 is from the library RPCI-1 constructed by the group of
          Pieter de Jong. For further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2.
FEATURES             Location/Qualifiers
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                     complement(AL596089.19:88763. .88922),
                     complement(AL596089.19:84634. .84815),
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                     complement(AL596089.19:15200. .15607))
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                     /note="match: ESTs: BF970104.1
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                     complement(AL596089.19:90194. .90375),
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                     complement(AL596089.19:83217. .83376),
                     complement(AL596089.19:79071. .79252),
                     complement(AL596089.19:77675. .77834),
                     complement(AL596089.19:74661. .74818),
                     complement(AL596089.19:73270. .73429),
                     complement(AL596089.19:70166. .70347),
                     complement(AL596089.19:68763. .68922),
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                     complement(AL596089.19:60853. .61012),
                     complement(AL596089.19:41107. .41288),
                     complement(AL596089.19:39742. .39901),
                     complement(AL596089.19:32195. .32376),
                     complement(AL596089.19:31506. .31654),
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                     complement(AL596089.19:16248. .16366),
                     complement(AL596089.19:15446. .15607))
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                     /note="match: proteins: P08519"
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                     PPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPH
                     SHSRTPEYYPNAGLIMNYCRNPDPVAAPYCYTRDPSVRWEYCNLTQCSDAEGTAVAPP
                     TITPIPSLEAPSEQAPTEQRPGVQECYHGNGQSYQGTYFITVTGRTCQAWSSMTPHSH
                     SRTPAYYPNAGLIKNYCRNPDPVAAPWCYTTDPSVRWEYCNLTRCSDAEWTAFVPPNV
                     ILAPSLEAFFEQALTEETPGVQDCYYHYGQSYRGTYSTTVTGRTCQAWSSMTPHQHSR
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                     EYYPNGGLTRNYCRNPDAEISPWCYTMDPNVRWEYCNLTQCPVTESSVLATSTAVSEQ
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                     PVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNP
                     DADTGPWCFTMDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGK
                     GYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYT
                     MNPRKLFDYCDIPLCASSSFDCGKPQVEPKKCPGSIVGGCVAHPHSWPWQVSLRTRFG
                     KHFCGGTLISPEWVLTAAHCLKKSSRPSSYKVILGAHQEVNLESHVQEIEVSRLFLEP
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                     PNKPGVYARVSRFVTWIEGMMRNN"
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                     /pseudo
     CDS             complement(join(16194. .16339,26376. .26489))
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                     /note="match: proteins: O18783 O46507 P00747 P06867 P06868
                     P12545 P20918 P80009 P80010 P81286 Q15146 Q29485 Q91WJ5
                     Q9R0W3"
                     /pseudo

  Query Match             92.8%;  Score 186.2;  DB 5;  Length 163599;
  Best Local Similarity   95.0%;  Pred. No. 1.1e-46;
  Matches  191;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Db      89012 TTGACGTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 89071

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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Db      89072 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 89131

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db      89132 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 89191

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      89192 GTCTTCACCCCACGCTGGTGA 89212


RESULT 6
AC010893/c
LOCUS       AC010893               177878 bp    DNA     linear   HTG 07-JUL-2000
DEFINITION  Homo sapiens chromosome 6 clone RP11-480A20, WORKING DRAFT
            SEQUENCE, 18 unordered pieces.
ACCESSION   AC010893
VERSION     AC010893.5  GI:8568869
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 177878)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 177878)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-SEP-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jun 16, 2000 this sequence version replaced gi:6850583.

            ---------------- Genome Center ----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0480A20
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 76%
            Sequencing vector: plasmid; 24%
            Chemistry: Dye-primer ET; 76% of reads
            Chemistry: Dye-terminator Big Dye; 24% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 165387 bases at least Q40
            Consensus quality: 170279 bases at least Q30
            Consensus quality: 172646 bases at least Q20
            Insert size: 183000; agarose-fp
            Insert size: 176178; sum-of-contigs
            Quality coverage: 4.11 in Q20 bases; agarose-fp
            Quality coverage: 4.01 in Q20 bases; sum-of-contigs
            -------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 18 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1046: contig of 1046 bp in length
            *     1047     1146: gap of unknown length
            *     1147     2235: contig of 1089 bp in length
            *     2236     2335: gap of unknown length
            *     2336     3349: contig of 1014 bp in length
            *     3350     3449: gap of unknown length
            *     3450     5172: contig of 1723 bp in length
            *     5173     5272: gap of unknown length
            *     5273     7349: contig of 2077 bp in length
            *     7350     7449: gap of unknown length
            *     7450     9861: contig of 2412 bp in length
            *     9862     9961: gap of unknown length
            *     9962    13599: contig of 3638 bp in length
            *    13600    13699: gap of unknown length
            *    13700    16835: contig of 3136 bp in length
            *    16836    16935: gap of unknown length
            *    16936    21649: contig of 4714 bp in length
            *    21650    21749: gap of unknown length
            *    21750    28521: contig of 6772 bp in length
            *    28522    28621: gap of unknown length
            *    28622    36556: contig of 7935 bp in length
            *    36557    36656: gap of unknown length
            *    36657    45767: contig of 9111 bp in length
            *    45768    45867: gap of unknown length
            *    45868    59019: contig of 13152 bp in length
            *    59020    59119: gap of unknown length
            *    59120    75610: contig of 16491 bp in length
            *    75611    75710: gap of unknown length
            *    75711    93797: contig of 18087 bp in length
            *    93798    93897: gap of unknown length
            *    93898   116372: contig of 22475 bp in length
            *   116373   116472: gap of unknown length
            *   116473   144933: contig of 28461 bp in length
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                     /db_xref="taxon:9606"
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     misc_feature    5273. .7349
                     /note="assembly_name:Contig54"
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     misc_feature    9962. .13599
                     /note="assembly_name:Contig56"
     gap             13600. .13699
                     /estimated_length=unknown
     misc_feature    13700. .16835
                     /note="assembly_name:Contig57"
     gap             16836. .16935
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     gap             28522. .28621
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     misc_feature    28622. .36556
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     misc_feature    36657. .45767
                     /note="assembly_name:Contig63"
     gap             45768. .45867
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     misc_feature    45868. .59019
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     misc_feature    59120. .75610
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     gap             75611. .75710
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     misc_feature    75711. .93797
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     misc_feature    93898. .116372
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     gap             116373. .116472
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                     /note="assembly_name:Contig68
                     clone_end:SP6
                     vector_side:right"
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                     /estimated_length=unknown
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                     /note="assembly_name:Contig69"
ORIGIN

  Query Match             92.8%;  Score 186.2;  DB 12;  Length 177878;
  Best Local Similarity   95.0%;  Pred. No. 1.1e-46;
  Matches  191;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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Db     171440 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 171381

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  ||||||||||||||||||||||||||||||||| |||||||||
Db     171380 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 171321

Qy        181 GTCTTCACCCCACGCTGGTGA 201
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Db     171320 GTCTTCACCCCACGCTGGTGA 171300


RESULT 7
AC084862/c
LOCUS       AC084862               179154 bp    DNA     linear   HTG 26-JUL-2005
DEFINITION  Papio anubis clone rp41-286p17, WORKING DRAFT SEQUENCE, 2 ordered
            pieces.
ACCESSION   AC084862
VERSION     AC084862.14  GI:59797159
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 179154)
  AUTHORS   Lau,C., Boffelli,D. and Roe,B.A.
  TITLE     Papio anubis BAC Clone rp41-286p17
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179154)
  AUTHORS   Lau,C., Boffelli,D. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-2000) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3  (bases 1 to 179154)
  AUTHORS   Lau,C., Boffelli,D. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2005) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Feb 15, 2005 this sequence version replaced gi:55701371.
            -------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1    68161: contig of 68161 bp in length
            *   68162    68261: gap of unknown length
            *   68262   179154: contig of 110893 bp in length.
FEATURES            Location/Qualifiers
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:9555"
                    /clone="rp41-286p17"
                    /clone_lib="RPCI - 41 Male (Olive) Baboon BAC Library"
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                    /estimated_length=unknown
ORIGIN

  Query Match             86.7%;  Score 174;  DB 12;  Length 179154;
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  Matches  183;  Conservative    1;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Db      75687 TTGACATCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATTCTACAAGGTCATCCTGGGTG 75628

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              ||||||||||||||    |||||| | |||||||||||||:||||| |||| | ||||||
Db      75627 CACACCAAGAAGTGCGTCTCGAACCACATGTTCAGGAAATAGAAGTATCTAAGATGTTCT 75568

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||| ||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db      75567 CGGAGCCCGCAGGAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 75508

Qy        181 GTCTTCACCCCACGCTGGTG 200
              |||||||||| | |||||||
Db      75507 GTCTTCACCCTATGCTGGTG 75488


RESULT 8
AC084863/c
LOCUS       AC084863               171010 bp    DNA     linear   HTG 26-JUL-2005
DEFINITION  Papio anubis clone rp41-339m12, WORKING DRAFT SEQUENCE, 2 ordered
            pieces.
ACCESSION   AC084863
VERSION     AC084863.24  GI:63028229
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 171010)
  AUTHORS   Lau,C., Boffelli,D. and Roe,B.A.
  TITLE     Papio anubis BAC Clone rp41-339m12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171010)
  AUTHORS   Lau,C., Boffelli,D. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-2000) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3  (bases 1 to 171010)
  AUTHORS   Lau,C., Boffelli,D. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2005) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On May 5, 2005 this sequence version replaced gi:62702059.
            -------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1    16952: contig of 16952 bp in length
            *   16953    17052: gap of unknown length
            *   17053   171010: contig of 153958 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9555"
                     /clone="rp41-339m12"
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     gap             16953. .17052
                     /estimated_length=unknown
ORIGIN

  Query Match           77.9%;  Score 156.2;  DB 12;  Length 171010;
  Best Local Similarity   91.6%;  Pred. No. 2.3e-37;
  Matches  164;  Conservative    1;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||||||||||||||||||||| |||||||||||| ||||| ||||||||||||||||
Db      20935 TTGACATCCTCATCTTTTCTAGGTTCTCAAGGCCTTCCTCCTATAAGGTCATCCTGGGTG 20876

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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RESULT 9
AC027197
LOCUS       AC027197               194321 bp    DNA     linear   HTG 24-AUG-2002
DEFINITION  Homo sapiens chromosome 6 clone RP11-189O14 map 6, LOW-PASS
            SEQUENCE SAMPLING.
ACCESSION   AC027197
VERSION     AC027197.3  GI:9887745
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 194321)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 6, clone RP11-189O14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 194321)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
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            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 194321)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
            FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
            Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
            Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
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Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Aug 24, 2000 this sequence version replaced gi:9799792.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-------------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-------------- Project Information
Center project name: L7625
Center clone name: 189_O_14
--------------.
* NOTE: This record contains 224 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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  Matches  154;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      45549 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAG 45583


RESULT 10
DD181590
LOCUS       DD181590               13869 bp    DNA     linear   PAT 19-DEC-2005
DEFINITION  LIPID-ASSOCIATED MOLECULES.
ACCESSION   DD181590
VERSION     DD181590.1  GI:83947781
KEYWORDS    JP 2005514007-A/10.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 13869)
  AUTHORS   Bhatia,U., Tang,T.Y., Elliott,V.S., Tran,U.K., Lee,S.Y., Chang,H.,
            Griffin,J.A., Zheng,W., Blake,J.J., Emerling,B.M., Lee,E.A.,
            Forsythe,I.J., Bulloch,S.A., Lee,S., Reddy,R., Khare,R.,
            Chawla,N.K., Baughn,M.R., Burrill,J.D., Ho,A. and Warren,B.A.
  TITLE     LIPID-ASSOCIATED MOLECULES
  JOURNAL   Patent: JP 2005514007-A 10 19-MAY-2005;
            INCYTE GENOMICS INC,Bridget A WARREN,Brooke M EMERLING, Ernestine A
            LEE, Hsin-Ru CHANG,Ian J FORSYTHE,Jennifer A GRIFFIN,Mariah R
            BAUGHN, Narinder K CHAWLA,Reena KHARE,Roopa REDDY,Sally LEE,Sean A
            BULLOCH, Soo Yeun LEE,Uyen K TRAN,Vicki S ELLIOTT,Tom Y TANG,Umesh
            BHATIA, John D BURRILL,Julie J BLAKE,Anne HO,Wenjin ZHENG
COMMENT     OS   Homo sapiens
            PN   JP 2005514007-A/10
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            PF   19-SEP-2002 JP 2003529924
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            18-DEC-2001 US    60/342166,22-JAN-2002 US    60/351262, PR
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            PI   brooke m emerling,ernestine a lee,ian j forsythe,sean a  PI
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ORIGIN
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  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

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Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321


RESULT 11
HSALIPOA
LOCUS       HSALIPOA               13938 bp    mRNA    linear   PRI 30-MAR-1995
DEFINITION  Human mRNA for apolipoprotein(a).
ACCESSION   X06290 M17399 X06696
VERSION     X06290.1  GI:28619
KEYWORDS    apolipoprotein; apolipoprotein A; glycoprotein; lipoprotein;
            plasminogen; serine protease.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 13938)
  AUTHORS   McLean,J.W., Tomlinson,J.E., Kuang,W.J., Eaton,D.L., Chen,E.Y.,
            Fless,G.M., Scanu,A.M. and Lawn,R.M.
  TITLE     cDNA sequence of human apolipoprotein(a) is homologous to
            plasminogen
  JOURNAL   Nature 330 (6144), 132-137 (1987)
   PUBMED   3670400
REFERENCE   2  (bases 1 to 13938)
  AUTHORS   McLean,J.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-1987) McLean J.W., Genentech Inc, 460 Point San
            Bruno Blvd, So. San Francisco CA 94080
FEATURES             Location/Qualifiers
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YCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYST
TVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYC
NLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTV
TGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDPVAAPYCYTRDPSVRWEYCNL
TQCSDAEGTAVAPPTITPIPSLEAPSEQAPTEQRPGVQECYHGNGQSYQGTYFITVTG
RTCQAWSSMTPHSHSRTPAYYPNAGLIKNYCRNPDPVAAPWCYTTDPSVRWEYCNLTR
CSDAEWTAFVPPNVILAPSLEAFFEQALTEETPGVQDCYYHYGQSYRGTYSTTVTGRT
CQAWSSMTPHQHSRTPENYPNAGLTRNYCRNPDAEIRPWCYTMDPSVRWEYCNLTQCL
VTESSVLATLTVVPDPSTEASSEEAPTEQSPGVQDCYHGDGQSYRGSFSTTVTGRTCQ
SWSSMTPHWHQRTTEYYPNGGLTRNYCRNPDAEISPWCYTMDPNVRWEYCNLTQCPVT
ESSVLATSTAVSEQAPTEQSPTVQDCYHGDGQSYRGSFSTTVTGRTCQSWSSMTPHWH
QRTTEYYPNGGLTRNYCRNPDAEIRPWCYTMDPSVRWEYCNLTQCPVMESTLLTTPTV
VPVPSTELPSEEAPTENSTGVQDCYRGDGQSYRGTLSTTITGRTCQSWSSMTPHWHRR
IPLYYPNAGLTRNYCRNPDAEIRPWCYTMDPSVRWEYCNLTRCPVTESSVLTTPTVAP
VPSTEAPSEQAPPEKSPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTP
ENYPNAGLTENYCRNPDSGKQPWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVP
SMEAHSEAAPTEQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPEN
YPNDGLTMNYCRNPDADTGPWCFTMDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSL
GPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYC
RNPDGDINGPWCYTMNPRKLFDYCDIPLCASSSFDCGKPQVEPKKCPGSIVGGCVAHP
HSWPWQVSLRTRFGKHFCGGTLISPEWVLTAAHCLKKSSRPSSYKVILGAHQEVNLES
HVQEIEVSRLFLEPTQADIALLKLSRPAVITDKVMPACLPSPDYMVTARTECYITGWG
ETQGTFGTGLLKEAQLLVIENEVCNHYKYICAEHLARGTDSCQGDSGGPLVCFEKDKY
ILQGVTSWGLGCARPNKPGVYARVSRFVTWIEGMMRNN"

sig_peptide	46. .102
	/note="signal peptide (AA -19 to -)"
mat_peptide	103. .13689
	/product="apolipoprotein (a) (AA 1- 4529)"
repeat_region	436. .7959
	/note="direct repeat region A (22x)"
repeat_region	7960. .8301
	/note="direct repeat B"
repeat_region	8302. .8985
	/note="direct repeat region A (2x)"
repeat_region	8986. .10011
	/note="direct repeat region B (3x)"
misc_feature	13911. .13916
	/note="polyA signal"
polyA_site	13938
	/note="polyA site"

ORIGIN

Query Match 72.0%; Score 144.4; DB 5; Length 13938;
Best Local Similarity 89.5%; Pred. No. 1.2e-33;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

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Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db      13150 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 13209

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db      13210 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 13269

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    |  ||| |  ||
Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321
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RESULT 12
AC093405/c

LOCUS	AC093405 150377 bp DNA linear HTG 27-SEP-2002
DEFINITION	Lemur catta, WORKING DRAFT SEQUENCE, 7 ordered pieces.
ACCESSION	AC093405
VERSION	AC093405.2 GI:23334717
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE	Lemur catta (ring-tailed lemur)
ORGANISM	Lemur catta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini; Lemuridae; Lemur.
REFERENCE	1 (bases 1 to 150377)
AUTHORS	Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M. and Cheng,J.-F.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 150377)
AUTHORS	Martin,J., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M. and Cheng,J.-F.F.
TITLE	Direct Submission
JOURNAL	Submitted (23-AUG-2001) Berkeley PGA, Lawrence Berkeley National Laboratory, 1 Cyclotron rd., Berkeley, CA 94720, United States of America
REFERENCE	3 (bases 1 to 150377)
AUTHORS	Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M. and Cheng,J.-F.
TITLE	Direct Submission
JOURNAL	Submitted (27-SEP-2002) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT	On Sep 27, 2002 this sequence version replaced gi:15281242. Draft Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: L004-139K21 Bac Clone Name:LB2-139K21 Additional information on comparative analysis and ordering are available at: http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value= Funding agent: Programs for Genomic Applications (NHLBI) Contact: 'Jody Schwartz' jrschwartz@lbl.gov Summary Statistics: Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye Assembly program: Phrap version 0.990329. * NOTE: This is a 'working draft' sequence. It currently

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            * consists of 7 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    10181: contig of 10181 bp in length
            *    10182    10281: gap of unknown length
            *    10282    35862: contig of 25581 bp in length
            *    35863    35962: gap of unknown length
            *    35963    55428: contig of 19466 bp in length
            *    55429    55528: gap of unknown length
            *    55529    64324: contig of 8796 bp in length
            *    64325    64424: gap of unknown length
            *    64425    77652: contig of 13228 bp in length
            *    77653    77752: gap of unknown length
            *    77753    84124: contig of 6372 bp in length
            *    84125    84224: gap of unknown length
            *    84225   150377: contig of 66153 bp in length.
FEATURES             Location/Qualifiers
     source          1. .150377
                     /organism="Lemur catta"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9447"
     gap             10182. .10281
                     /estimated_length=unknown
     gap             35863. .35962
                     /estimated_length=unknown
     gap             55429. .55528
                     /estimated_length=unknown
     gap             64325. .64424
                     /estimated_length=unknown
     gap             77653. .77752
                     /estimated_length=unknown
     gap             84125. .84224
                     /estimated_length=unknown
ORIGIN

  Query Match             71.9%;  Score 144.2;  DB 12;  Length 150377;
  Best Local Similarity   85.2%;  Pred. No. 1.2e-33;
  Matches  161;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          13 TCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAG 72
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Db       59197 TCTTTCCTAGGTCCCGATGGCCTTCAGCATACAGGGTCATCCTGGGCGCACACGAAGAAA 59138

Qy          73 TGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACAC 132
               ||| ||| ||||  |||||||| |||| |||||||||||||||||||||||||||||| |
Db       59137 AGAATCTCCAATCAGATGTTCAGCAAATCGAAGTGTCTAGGCTGTTCTTGGAGCCCACCC 59078

Qy         133 AAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTGGTCTTCACCCCA 192
               |||||| |||||||||| |||||||||||||||| |||||| |||||| ||  ||| |
Db       59077 GAGCAGACATTGCCTTGCTGAAGCTAAGCAGGTACTGGCTCACTTGTGGTTTTTGCCCTA 59018

Qy         193 CGCTGGTGA 201
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Db       59017 AGCTGGTGA 59009


RESULT 13
AX815991
LOCUS       AX815991                744 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 64 from Patent WO03066842.
ACCESSION   AX815991
VERSION     AX815991.1  GI:39646630
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Susilo,R., Korting,H.C., Gassen,H.G., Hils,M. and Pasternack,R.
  TITLE     Method for producing recombinant proteins in micro-organisms
  JOURNAL   Patent: WO 03066842-A 64 14-AUG-2003;
            Trommsdorff GmbH & Co.KG Arzneimittel (DE)
FEATURES             Location/Qualifiers
     source          1. .744
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 744;
  Best Local Similarity   85.0%;  Pred. No. 6.1e-30;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy           8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
               || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db         174 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 233

Qy          68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
               ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db         234 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 293

Qy         128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
               ||||| |  |||||||||||||||||||||||||      |  ||| |  ||
Db         294 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 346


RESULT 14
AX463624
LOCUS       AX463624                750 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 3 from Patent WO0250290.
ACCESSION   AX463624
VERSION     AX463624.1  GI:21886384
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagai,N., Laroche,Y. and Collen,D.J.
  TITLE     A yeast expression vector and a method of making a recombinant
            protein by expression in a yeast cell
  JOURNAL   Patent: WO 0250290-A 3 27-JUN-2002;
            THROMB X NV (BE)
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             <1. .750
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD42144.1"
                     /db_xref="GI:21886385"
                     /translation="APSFDCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRFGMH
                     FCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTR
                     KDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGLLKEAQL
                     PVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTS
                     WGLGCARPNKPGVYVRVSRFVTWIEGVMRNN"
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 750;
  Best Local Similarity   85.0%;  Pred. No. 6.1e-30;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy           8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
               || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db         180 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 239

Qy          68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
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                ||||||||| |||||| | |||||||||||||:||||||||||||||||||||||||
Db        240 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 299

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                ||||| |  |||||||||||||||||||||||||||     |  ||| |  ||
Db        300 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 352


RESULT 15
AX815990
LOCUS       AX815990                750 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 63 from Patent WO03066842.
ACCESSION   AX815990
VERSION     AX815990.1  GI:39646629
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Susilo,R., Korting,H.C., Gassen,H.G., Hils,M. and Pasternack,R.
  TITLE     Method for producing recombinant proteins in micro-organisms
  JOURNAL   Patent: WO 03066842-A 63 14-AUG-2003;
            Trommsdorff GmbH & Co.KG Arzneimittel (DE)
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 750;
  Best Local Similarity   85.0%;  Pred. No. 6.1e-30;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db        180 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 239

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
                |||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||
Db        240 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 299

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                ||||| |  |||||||||||||||||||||||||||     |  ||| |  ||
Db        300 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 352


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GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 13:01:40 ; Search time 4486 Seconds
(without alignments)
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Title: US-10-796-280-19350
Perfect score: 200.6
Sequence: 1 ttgacatcctcatcttttct.....tcttcaccccacgctggtga 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	134.2	66.9	2141	14	DQ048566	DQ048566 Pan trogl
	2	134.2	66.9	2798	6	CR859622	CR859622 Pongo pyg
	3	132.6	66.1	424	10	H73861	H73861 ys12a02.r1
	4	132.6	66.1	433	10	H90220	H90220 yu85g08.r1
	5	132.6	66.1	459	10	R94305	R94305 yq41c07.r1
c	6	132.6	66.1	466	1	AI948806	AI948806 wq26e12.x
	7	132.6	66.1	475	10	N91337	N91337 za14h05.r1
	8	132.6	66.1	481	10	H60805	H60805 yr45g09.r1
	9	132.6	66.1	517	4	CB162370	CB162370 K-EST0222
	10	132.6	66.1	543	4	CB161910	CB161910 K-EST0221
	11	132.6	66.1	564	4	CB161593	CB161593 K-EST0221
	12	132.6	66.1	594	1	AV661991	AV661991 AV661991
	13	132.6	66.1	611	1	AV662084	AV662084 AV662084
	14	132.6	66.1	766	2	BI759134	BI759134 603042546
	15	132.6	66.1	859	2	BG402207	BG402207 602465764
c	16	132.6	66.1	862	4	BX453606	BX453606 BX453606
	17	132.6	66.1	2141	14	DQ048565	DQ048565 Homo sapi
	18	132.6	66.1	4634	6	CR749293	CR749293 Homo sapi
	19	131.6	65.6	752	4	BX105247	BX105247 BX105247
	20	131.4	65.5	368	10	H95494	H95494 yv13f06.r1
	21	131	65.3	526	5	CD608134	CD608134 56072712H
	22	131	65.3	526	5	CD608136	CD608136 56072820H
	23	123.6	61.6	580	9	DA635394	DA635394 DA635394
c	24	123	61.3	700	7	BB884891	BB884891 BB884891
	25	123	61.3	984	8	CO581599	CO581599 ILLUMIGEN
	26	123	61.3	991	8	CO580006	CO580006 ILLUMIGEN
	27	121.6	60.6	686	4	BX498968	BX498968 DKFZp779N
c	28	120	59.8	1042	1	AL579900	AL579900 AL579900
	29	118.2	58.9	589	10	H73871	H73871 ys14d05.r1
c	30	115.8	57.7	744	7	BB893901	BB893901 BB893901
c	31	113.4	56.5	766	1	AV700701	AV700701 AV700701
c	32	110.2	54.9	768	7	BB879859	BB879859 BB879859
	33	105.8	52.7	360	1	AV654539	AV654539 AV654539
	34	105.8	52.7	606	1	AV662061	AV662061 AV662061
	35	104.4	52.0	707	9	DR102991	DR102991 JHU008B07
	36	97.8	48.8	611	1	AV662095	AV662095 AV662095
	37	94.8	47.3	568	2	BF970104	BF970104 602272382
c	38	92.4	46.1	782	1	AL531542	AL531542 AL531542
c	39	91.6	45.7	525	11	BH276396	BH276396 CH230-108
	40	90.8	45.3	815	10	DR773354	DR773354 ILLUMIGEN
	41	89.2	44.5	765	4	BX922138	BX922138 BX922138
	42	87.6	43.7	659	5	CJ003205	CJ003205 CJ003205
	43	87.6	43.7	724	4	BX922039	BX922039 BX922039
	44	87.6	43.7	764	4	BX921618	BX921618 BX921618
	45	87.6	43.7	864	3	BP447197	BP447197 BP447197

ALIGNMENTS

RESULT 1
DQ048566
LOCUS DQ048566 2141 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes PLG gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ048566
VERSION DQ048566.1 GI:66901765
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2141)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 2141)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .2141
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1. .>2141
/gene="PLG"
/locus_tag="HC16515"
ORIGIN

Query Match 66.9%; Score 134.2; DB 14; Length 2141;

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  Best Local Similarity   85.5%;  Pred. No. 9.9e-32;
  Matches  148;  Conservative    1;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db       1571 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1630

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db       1631 AGAAGTGAAGCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1690

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| | ||||||||||||||||||||||||||||    |  ||| |  ||
Db       1691 CACACGAACAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCATCATCACTG 1743


RESULT 2
CR859622
LOCUS       CR859622               2798 bp    mRNA    linear   HTC 17-APR-2005
DEFINITION  Pongo pygmaeus mRNA; cDNA DKFZp470G2422 (from clone DKFZp470G2422).
ACCESSION   CR859622
VERSION     CR859622.1  GI:55730119
KEYWORDS    HTC.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 2798)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFZp470G2422) is available at
            the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
            Berlin, Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp470G2422
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .2798
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp470G2422"
                     /tissue_type="liver"
                     /clone_lib="470 (synonym: plivl). Vector pSport1_Sfi; host
                     DH10B; sites SfilA + SfilB"
                     /dev_stage="adult"
                     /note="plasmin (Homo sapiens)"
     gene            1. .2798
                     /gene="DKFZp470G2422"
     CDS             34. .2466
                     /gene="DKFZp470G2422"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="CAH91784.1"
                     /db_xref="GI:55730120"
                     /db_xref="GOA:Q5R8X6"
                     /db_xref="InterPro:IPR000001"
                     /db_xref="InterPro:IPR001254"
                     /db_xref="InterPro:IPR001314"
                     /db_xref="InterPro:IPR003014"
                     /db_xref="InterPro:IPR003609"
                     /db_xref="InterPro:IPR003966"
                     /db_xref="InterPro:IPR011358"
                     /db_xref="UniProtKB/TrEMBL:Q5R8X6"
                     /translation="MEHKEVVLLLLLFLKSGQGEPLDDYVNTQGASLFSVTKKQLRAG
                     SIEECAAKCEEEKEFTCRAFQYHSKEQQCVIMAENRKSSIIIRMRDVVLFEKKVYLSE
                     CKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDAQ
                     GPWCYTTDPEHRYDYCDIPECEEACMHCSGENYDGKISKTMSGLECQAWDSQSPHAHG
                     YIPSKFPNKNLKKNYCRNPDGEPRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCL
                     KGTGENYRGNVAVTVSGHTCQRWSAQTPQTHNRTPENFPCKNLDENYCRNPDGEKAPW
                     CYTTNSQVRWEYCKIPSCGSSPVSTEQLDPTAPPELTPVVQDCYHGDGQSYRGTSSTT
                     TTGKKCQSWSSMTPHWHQKTPENYPDAGLTMNYCRNPDADKGPWCFTTDPSVRWEYCN
                     LKKCSGTEGSVVAPPPVVQLPNVETPSEEDCMFGNGKGYRGKRATTVTGTPCQEWAAQ
                     EPHRHSIFTPQTNPRAGLEKNYCRNPDGDEGGPWCYTTNPRKHYDYCDVPQCASSSFD
                     CGKPQVEPKKCPGRVVGGCVANAHSWPWQVSLRTRFGTHFCGGTLISPEWVLTAAHCL
                     EKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTRADIALLKLSSPAVITDKVI
                     PACLPSPNYVVAGRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVK
                     STELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSR
                     FVTWIEGVMRNN"
ORIGIN

  Query Match             66.9%;  Score 134.2;  DB 6;  Length 2798;
  Best Local Similarity   85.5%;  Pred. No. 1.1e-31;
  Matches  148;  Conservative    1;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db       1896 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1955

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| || ||| | |||||||||||||:|||||||||||||||||||||||||||
Db       1956 AGAAGTGAATCTTGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2015

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |||||||||||||||||||||||||||||     |  ||| |  ||
Db       2016 CACACGAGCAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCTGTCATCACTG 2068


RESULT 3
H73861
LOCUS       H73861                 424 bp    mRNA    linear   EST 31-OCT-1995
DEFINITION  ys12a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:214538 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   H73861
VERSION     H73861.1  GI:1046795
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  PUBMED    8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1035
            High quality sequence stops: 330
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1035   Std Error: 0.00
            Seq primer: M13RP1
```

High quality sequence stop: 330.

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FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:214538"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
```

Query Match 66.1%; Score 132.6; DB 10; Length 424;
Best Local Similarity 85.0%; Pred. No. 2.1e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

```
Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db        150 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 209

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db        210 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 269

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||     |  ||| |  ||
Db        270 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 322
```

```
RESULT 4
H90220
LOCUS       H90220                  433 bp    mRNA    linear   EST 28-NOV-1995
DEFINITION  yu85g08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:240638 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   H90220
VERSION     H90220.1  GI:1080650
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1021
            High quality sequence stops: 355
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1021   Std Error: 0.00
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Seq primer: M13RP1
High quality sequence stop: 355.

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FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3789771"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:240638"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
```

Query Match 66.1%; Score 132.6; DB 10; Length 433;
Best Local Similarity 85.0%; Pred. No. 2.1e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

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Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db         36 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 95

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db         96 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 155

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||     |  ||| |  ||
Db        156 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 208
```

```
RESULT 5
R94305
LOCUS       R94305                  459 bp    mRNA    linear   EST 30-AUG-1995
DEFINITION  yq41c07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:198348 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   R94305
VERSION     R94305.1  GI:969700
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1004
            High quality sequence stops: 293
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
```

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1004 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 293.

FEATURES Location/Qualifiers
source 1. .459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3767398"
/db_xref="taxon:9606"
/clone="IMAGE:198348"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 66.1%; Score 132.6; DB 10; Length 459;
Best Local Similarity 85.0%; Pred. No. 2.1e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
|| | ||| | |||| ||||||||||||||||||||||||||||||||||||||||||
Db 54 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 113

Qy 68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||
Db 114 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 173

Qy 128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
||||| | |||||||||||||||||||||||||| | ||| | ||
Db 174 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 226

RESULT 6
AI948806/c
LOCUS AI948806 466 bp mRNA linear EST 08-MAR-2000
DEFINITION wq26e12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472430 3' similar to gb:X05199 PLASMINOGEN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI948806
VERSION AI948806.1 GI:5741116
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 535 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 430.

FEATURES Location/Qualifiers
source 1. .466
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2472430"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 66.1%; Score 132.6; DB 1; Length 466;
Best Local Similarity 85.0%; Pred. No. 2.1e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
|| | ||| | |||| ||||||||||||||||||||||||||||||||||||||||||
Db 246 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 187

Qy 68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||
Db 186 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 127

Qy 128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
||||| | |||||||||||||||||||||||||| | ||| | ||
Db 126 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 74

RESULT 7
N91337
LOCUS N91337 475 bp mRNA linear EST 03-APR-1996
DEFINITION za14h05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292569 5' similar to gb:X05199 PLASMINOGEN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION N91337
VERSION N91337.1 GI:1444664
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 475)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 296.

FEATURES Location/Qualifiers
source 1. .475
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="GDB:3800346"
/db_xref="taxon:9606"
/clone="IMAGE:292569"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 66.1%; Score 132.6; DB 10; Length 475;
Best Local Similarity 85.0%; Pred. No. 2.1e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

```
Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db         32 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 91

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||:||||||||||||||||||||||||||||
Db         92 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 151

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  | ||||||||||||||||||||||||||||     |  ||| |  ||
Db        152 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 204
```

RESULT 8
H60805
LOCUS H60805 481 bp mRNA linear EST 06-OCT-1995
DEFINITION yr45g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208288 5' similar to gb:X05199 PLASMINOGEN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION H60805
VERSION H60805.1 GI:1013637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 481)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 339
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 339.
FEATURES Location/Qualifiers
source 1. .481
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3777419"
/db_xref="taxon:9606"
/clone="IMAGE:208288"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 66.1%; Score 132.6; DB 10; Length 481;
Best Local Similarity 85.0%; Pred. No. 2.1e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

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Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db        133 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 192

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db        193 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 252

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  | ||||||||||||||||||||||||||||     |  ||| |  ||
Db        253 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 305
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RESULT 9
CB162370
LOCUS CB162370 517 bp mRNA linear EST 30-JAN-2003
DEFINITION K-EST0222936 L17N670205n1 Homo sapiens cDNA clone L17N670205n1-42-H08 5', mRNA sequence.
ACCESSION CB162370
VERSION CB162370.1 GI:28148496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 517)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 42 row: H column: 08
High quality sequence stop: 517.
FEATURES Location/Qualifiers
source 1. .517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L17N670205n1-42-H08"
/sex="F"
/lab_host="Top10F'"
/clone_lib="L17N670205n1"
/note="Organ: Liver; Vector: pT7T3D-PacI; Site_1: EcoRI;

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                Site_2: NotI; The library was contributed by the Soares
                laboratory and it was constructed as described by Bonaldo,
                M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                6(9): 791-806. RNA was prepared from harvested cell
                culture."
ORIGIN

  Query Match            66.1%;  Score 132.6;  DB 4;  Length 517;
  Best Local Similarity  85.0%;  Pred. No. 2.2e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db        258 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 317

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||||:||||||||||||||||||||||||||
Db        318 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 377

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||      |  ||| |  ||
Db        378 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 430


RESULT 10
CB161910
LOCUS       CB161910                  543 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  K-EST0221967 L17N670205n1 Homo sapiens cDNA clone
            L17N670205n1-41-G11 5', mRNA sequence.
ACCESSION   CB161910
VERSION     CB161910.1  GI:28148036
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 543)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 41  row: G  column: 11
            High quality sequence stop: 543.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L17N670205n1-41-G11"
                     /sex="F"
                     /lab_host="Top10F'"
                     /clone_lib="L17N670205n1"
                     /note="Organ: Liver; Vector: pT7T3D-PacI; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
ORIGIN

  Query Match            66.1%;  Score 132.6;  DB 4;  Length 543;
  Best Local Similarity  85.0%;  Pred. No. 2.2e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
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Db        283 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 342

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||||:||||||||||||||||||||||||||
Db        343 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 402

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||      |  ||| |  ||
Db        403 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 455


RESULT 11
CB161593
LOCUS       CB161593                  564 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  K-EST0221565 L17N670205n1 Homo sapiens cDNA clone
            L17N670205n1-35-F05 5', mRNA sequence.
ACCESSION   CB161593
VERSION     CB161593.1  GI:28147719
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 35  row: F  column: 05
            High quality sequence stop: 564.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /sex="F"
                     /lab_host="Top10F'"
                     /clone_lib="L17N670205n1"
                     /note="Organ: Liver; Vector: pT7T3D-PacI; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
ORIGIN

  Query Match            66.1%;  Score 132.6;  DB 4;  Length 564;
  Best Local Similarity  85.0%;  Pred. No. 2.2e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db        164 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 223

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||||:||||||||||||||||||||||||||
Db        224 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 283

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||      |  ||| |  ||
Db        284 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 336
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RESULT 12
AV661991
LOCUS       AV661991                 594 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  AV661991 GLC Homo sapiens cDNA clone GLCGZG06 3', mRNA sequence.
ACCESSION   AV661991
VERSION     AV661991.1  GI:9883005
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCGZG06"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 1;  Length 594;
  Best Local Similarity   85.0%;  Pred. No. 2.3e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db        123 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 182

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db        183 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 242

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||      |  ||| |  ||
Db        243 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 295


RESULT 13
AV662084
LOCUS       AV662084                 611 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  AV662084 GLC Homo sapiens cDNA clone GLCHAG06 3', mRNA sequence.
ACCESSION   AV662084
VERSION     AV662084.1  GI:9883098
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 611)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .611
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCHAG06"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 1;  Length 611;
  Best Local Similarity   85.0%;  Pred. No. 2.3e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db        122 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 181

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db        182 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 241

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||      |  ||| |  ||
Db        242 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 294


RESULT 14
BI759134
LOCUS       BI759134                 766 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603042546F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183003 5',
            mRNA sequence.
ACCESSION   BI759134
VERSION     BI759134.1  GI:15750712
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

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            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11456  row: l  column: 12
           High quality sequence stop: 766.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5183003"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 766;
  Best Local Similarity   85.0%;  Pred. No. 2.4e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db        258 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 317

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db        318 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 377

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db        378 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 430


RESULT 15
BG402207
LOCUS       BG402207                 859 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602465764F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4594023 5',
            mRNA sequence.
ACCESSION   BG402207
VERSION     BG402207.1  GI:13295655
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 859)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1334  row: o  column: 16
           High quality sequence stop: 629.
FEATURES             Location/Qualifiers
     source          1. .859
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4594023"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 859;
  Best Local Similarity   85.0%;  Pred. No. 2.5e-31;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db        313 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 372

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db        373 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 432

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db        433 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 485


Search completed: May 26, 2006, 16:10:41
Job time : 4490 secs
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GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 12:35:58 ; Search time 354 Seconds
(without alignments)
3958.819 Million cell updates/sec

Title: US-10-796-280-19350
Perfect score: 200.6
Sequence: 1 ttgacatcctcatctttttct.....tcttcaccccacgctggtga 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144.4	72.0	201	13	ADQ45134	Adq45134 Myocardia
2	144.4	72.0	201	13	ADQ45152	Adq45152 Myocardia
3	144.4	72.0	820	5	AAS80437	Aas80437 DNA encod
4	144.4	72.0	820	5	AAS66111	Aas66111 DNA encod
5	144.4	72.0	3756	13	ADQ38544	Adq38544 Human SNP
6	144.4	72.0	10422	8	ACA64741	Aca64741 Apolipopr
7	144.4	72.0	10422	10	ADF43405	Adf43405 Apolipopr
8	144.4	72.0	10422	14	AEA03076	Aea03076 iNOS nucl
9	144.4	72.0	13869	10	ACC49787	Acc49787 Human lip
10	144.4	72.0	13938	8	ACC47280	Acc47280 Human apo
11	144.4	72.0	13938	12	ADO33412	Ado33412 Human apo
12	144.4	72.0	13938	12	ADQ75139	Adq75139 Human apo
13	144.4	72.0	13938	13	ADQ38545	Adq38545 Human SNP
c 14	132.8	66.2	2178	5	AAS80436	Aas80436 DNA encod
15	132.6	66.1	744	10	ACH00783	Ach00783 Human mic
16	132.6	66.1	750	6	ABN89460	Abn89460 Human mic
17	132.6	66.1	750	10	ACH00782	Ach00782 Human mic
18	132.6	66.1	750	13	ADS20373	Ads20373 Human mic
19	132.6	66.1	783	10	ACH00781	Ach00781 Human mic
20	132.6	66.1	786	10	ACH00780	Ach00780 Human mic
21	132.6	66.1	999	10	ACH00777	Ach00777 Human-S c
22	132.6	66.1	1005	10	ACH00775	Ach00775 Human-S c
23	132.6	66.1	1011	10	ACH00778	Ach00778 Human-S c
24	132.6	66.1	1017	10	ACH00776	Ach00776 Human-S c
25	132.6	66.1	1038	10	ACH00773	Ach00773 Human-S c
26	132.6	66.1	1041	10	ACH00771	Ach00771 Human-S c
27	132.6	66.1	1047	6	ABN89461	Abn89461 Human min
28	132.6	66.1	1047	10	ACH00779	Ach00779 Human min
29	132.6	66.1	1047	13	ADS20377	Ads20377 Human min
30	132.6	66.1	1050	10	ACH00774	Ach00774 Human-S c
31	132.6	66.1	1053	10	ACH00772	Ach00772 Human-S c
32	132.6	66.1	1302	10	ACH00769	Ach00769 Human-S c
33	132.6	66.1	1314	10	ACH00770	Ach00770 Human-S c
34	132.6	66.1	1724	2	AAQ40318	Aaq40318 Sequence
35	132.6	66.1	1907	8	ACC51086	Acc51086 Human Pla
36	132.6	66.1	2145	10	ACH00785	Ach00785 Human Lys
37	132.6	66.1	2296	2	AAQ40258	Aaq40258 Plasmid p
38	132.6	66.1	2296	3	AAA89829	Aaa89829 Plasminog
39	132.6	66.1	2296	4	AAS12747	Aas12747 Plasmid p
40	132.6	66.1	2376	10	ACH00784	Ach00784 Human Glu
41	132.6	66.1	2376	13	ADS20379	Ads20379 Human pla
42	132.6	66.1	2400	10	ACH00752	Ach00752 Human-S c
43	132.6	66.1	2412	10	ACH00753	Ach00753 Human-S c
44	132.6	66.1	2430	10	ABX15877	Abx15877 DNA encod
45	132.6	66.1	2432	14	AED76372	Aed76372 Human pla

ALIGNMENTS

RESULT 1
ADQ45134
ID ADQ45134 standard; DNA; 201 BP.
XX
AC ADQ45134;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6797.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 6797; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 53 A; 54 C; 45 G; 48 T; 0 U; 1 Other;

Query Match 72.0%; Score 144.4; DB 13; Length 201;
Best Local Similarity 90.1%; Pred. No. 5.1e-40;
Matches 155; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db          9 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    |  ||| |  ||
Db        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 180
```

RESULT 2
ADQ45152
ID ADQ45152 standard; DNA; 201 BP.
XX
AC ADQ45152;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6815.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 6815; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 53 A; 54 C; 45 G; 48 T; 0 U; 1 Other;

Query Match 72.0%; Score 144.4; DB 13; Length 201;
Best Local Similarity 90.1%; Pred. No. 5.1e-40;
Matches 155; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db          9 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    |  ||| |  ||
Db        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 180
```

RESULT 3
AAS80437
ID AAS80437 standard; cDNA; 820 BP.
XX
AC AAS80437;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #16241.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX

PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG16250.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 16241; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 820 BP; 209 A; 203 C; 209 G; 199 T; 0 U; 0 Other;

Query Match 72.0%; Score 144.4; DB 5; Length 820;
Best Local Similarity 89.5%; Pred. No. 9.7e-40;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

```
Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db        116 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 175

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        176 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 235

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    | ||| |  ||
Db        236 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 287
```

RESULT 4
AAS66111
ID AAS66111 standard; cDNA; 820 BP.
XX
AC AAS66111;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #1915.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG01924.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 1915; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 820 BP; 209 A; 203 C; 209 G; 199 T; 0 U; 0 Other;

Query Match 72.0%; Score 144.4; DB 5; Length 820;
Best Local Similarity 89.5%; Pred. No. 9.7e-40;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

```
Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db        116 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 175

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        176 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 235

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    | ||| |  ||
Db        236 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 287
```

RESULT 5
ADQ38544
ID ADQ38544 standard; DNA; 3756 BP.

XX
AC ADQ38544;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 207.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
DR P-PSDB; ADQ39372.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 207; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 3756 BP; 1017 A; 965 C; 914 G; 839 T; 0 U; 21 Other;

Query Match 72.0%; Score 144.4; DB 13; Length 3756;
Best Local Similarity 90.1%; Pred. No. 1.9e-39;
Matches 155; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
Db 2968 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 3027

Qy 69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
Db 3028 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 3087

Qy 129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
Db 3088 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 3139

RESULT 6
ACA64741
ID ACA64741 standard; DNA; 10422 BP.
XX
AC ACA64741;
XX
DT 18-JUN-2003 (first entry)
XX
DE Apolipoprotein gene #1.
XX
KW Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer;
KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW tumouricidal immunocyte; antitumour.
XX
OS Unidentified.
XX
PN US2002177551-A1.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2001US-00870759.
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2003-361759/34.
DR P-PSDB; ABU79139.
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumor associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX
PS Example 2; Page; 167pp; English.
XX
CC The invention relates to a mammalian cell receptor, useful in the
CC treatment of cancer, which binds to tumour associated lipids and induces
CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC (by allowing tumour associated lipids to contact immunocytes in which
CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC deleted), a construct useful in the treatment of cancer comprising a
CC superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell
CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidally
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,

```
CC   and administering APCs to the host), producing a tumouricidal T cell
CC   population ex vivo in a mammal) by allowing a tumour associated lipids to
CC   contact T cells, in which adaptor proteins, which inhibit T cell
CC   activation by tumour associated antigens, are deleted or functionally
CC   deactivated to produce a tumouricidal population of T cells, and
CC   administering the tumouricidally activated T cells to the host, or
CC   allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC   administering the tumouricidally activated T cells to the host), treating
CC   (M5) cancer in a mammal (by administering a lipid binding molecule which
CC   binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC   a tumouricidal T cell population in vivo in a mammal (by allowing a
CC   tumour associated antigen to contact immunocytes in which adaptor
CC   proteins which inhibit T cell activation by tumour associated antigens
CC   are deleted or functionally deactivated) and producing (M7) a
CC   tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC   superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC   receptors, methods and compositions are useful for treating cancers and
CC   tumours. Bacterial superantigens are co-administered or administered as
CC   fusion constructs with anti-tumour proteins or motifs. The present
CC   sequence encodes an anti-tumour protein which is co-administered with or
CC   incorporated into a fusion construct with a superantigen. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from the US patnet
CC   office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ   Sequence 10422 BP; 3020 A; 2386 C; 2503 G; 2513 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 144.4;  DB 8;  Length 10422;
  Best Local Similarity   89.5%;  Pred. No. 3.1e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db       9634 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 9693

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db       9694 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 9753

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    |  ||| |  ||
Db       9754 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 9805


RESULT 7
ADF43405
ID   ADF43405 standard; DNA; 10422 BP.
XX
AC   ADF43405;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Apolipoprotein polynucleotide seqid 125.
XX
KW   receptor; lipid-based tumour associated antigen; cytostatic;
KW   antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW   infectious disease; apolipoprotein; ds.
XX
OS   Unidentified.
XX
PN   US2003157113-A1.
XX
PD   21-AUG-2003.
XX
PF   28-DEC-2000; 2000US-00751708.
XX
PR   28-DEC-1999;   99US-0173371P.
XX
PA   (TERM/) TERMAN D S.
XX
PI   Terman DS;
XX
DR   WPI; 2003-787326/74.
DR   P-PSDB; ADF43406.
XX
PT   New receptor in a mammalian cell that inhibits regular activation by
PT   receptors specific for lipid-based tumor associated antigens, useful for
PT   treating a neoplastic disease or tumor, and infectious diseases.
XX
PS   Example 3; SEQ ID NO 125; 151pp; English.
XX
CC   The invention describes a receptor in a mammalian cell that inhibits
CC   regular activation by receptors specific for lipid-based tumour
CC   associated antigen. The receptor has cytostatic and antimicrobial
CC   properties and is suitable for use in gene therapy. The receptors,
CC   methods and compositions are useful for treating a neoplastic disease or
CC   tumour (cancer), and infectious diseases. This sequence represents
CC   apolipoprotein polynucleotide, a cell surface moiety, the DNA of which
CC   can be transfected into a cell with superantigen DNA to generate
CC   antitumour immunity.
XX
SQ   Sequence 10422 BP; 3020 A; 2386 C; 2503 G; 2513 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 144.4;  DB 10;  Length 10422;
  Best Local Similarity   89.5%;  Pred. No. 3.1e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db       9634 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 9693

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db       9694 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 9753

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    |  ||| |  ||
Db       9754 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 9805


RESULT 8
AEA03076
ID   AEA03076 standard; DNA; 10422 BP.
XX
AC   AEA03076;
XX
DT   28-JUL-2005  (first entry)
XX
DE   iNOS nucleotide sequence SEQ ID NO:102.
XX
KW   tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW   inducible nitric oxide synthase; gene; ds.
XX
OS   Unidentified.
XX
PN   US2005112141-A1.
XX
PD   26-MAY-2005.
XX
PF   08-SEP-2004; 2004US-00937758.
XX
PR   30-AUG-2000; 2000US-00650884.
XX
PA   (TERM/) TERMAN D S.
XX
PI   Terman DS;
XX
DR   WPI; 2005-394926/40.
DR   P-PSDB; AEA03077.
XX
PT   New composition for treating a tumor or neoplastic disease in a subject
PT   comprises conjugates comprising superantigen polypeptides or nucleic
PT   acids with other molecules that produce a tumoricidal response.
XX
PS   Example 3; SEQ ID NO 102; 125pp; English.
XX
```

```
CC   The invention relates to a composition for treating a tumor or neoplastic
CC   disease in a subject. Also described: (1) a mammalian cell comprising an
CC   exogenous nucleic acid encoding a superantigen expressed in the cell,
CC   which cell also produces or expresses all alpha-anomers of
CC   monoglycosylceramide or diglycosylceramide, where expression of the
CC   superantigen and the mono- or diglycosylceramide is capable of eliciting
CC   an antitumor immune response in a mammal into which the cell is
CC   introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
CC   preparing a population of immunotherapeutic T or natural killer T (NKT)
CC   cells useful to treat a tumor or neoplastic disease in a subject; (4) an
CC   apoptotic cell preparation or lysate useful for treating a tumor or
CC   neoplastic disease in a subject, comprising a cell population that has
CC   been transfected with naked DNA encoding a superantigen, and treated to
CC   undergo apoptosis or lysis; and (5) a cell that has ingested or been
CC   transfected with the above apoptotic preparation or lysate, thus,
CC   rendering the cell effective in presenting material expressed from
CC   transfecting nucleic acid or material ingested to the immune system of a
CC   mammal to elicit an anti-tumor immune response. The composition and
CC   methods are useful for treating tumors or neoplastic diseases. The
CC   present sequence represents an iNOS nucleotide sequence, which is used in
CC   an example from the present invention. Note - The sequence data for this
CC   patent is not represented in the printed specification, but was obtained
CC   in electronic format directly from the USPTO web site.
XX
SQ   Sequence 10422 BP; 3020 A; 2386 C; 2503 G; 2513 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 144.4;  DB 14;  Length 10422;
  Best Local Similarity   89.5%;  Pred. No. 3.1e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9634 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 9693

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||.|||||||||||||||||||:|||||||||||||||||||||||||||||
Db       9694 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 9753

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||    |  ||| |  ||
Db       9754 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 9805


RESULT 9
ACC49787
ID   ACC49787 standard; cDNA; 13869 BP.
XX
AC   ACC49787;
XX
DT   10-JUL-2003  (first entry)
XX
DE   Human lipid-associated molecule LIPAM-10 encoding cDNA SEQ ID NO:27.
XX
KW   Human; lipid-associated molecule; LIPAM; cytostatic; cerebroprotective;
KW   antiarteriosclerotic; anti-HIV; antiallergic; antiparkinsonian; cardiant;
KW   anticonvulsant; nootropic; antiinflammatory; antiulcer; hepatotropic;
KW   antibacterial; virucide; protozoacide; antiparasitic; antilipaemic; AIDS;
KW   gene therapy; cell proliferative disease; cancer; atherosclerosis; ulcer;
KW   autoimmune disease; inflammatory disease; allergy; neurological disorder;
KW   stroke; Parkinson's disease; epilepsy; gastrointestinal disorder;
KW   cirrhosis; cardiovascular disorder; myocardial infarction; obesity;
KW   metabolic disorder; developmental disorder; endocrine disorder;
KW   pulmonary disorder; infection; lipid metabolism disorder; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             46. .13692
FT                   /*tag= a
FT                   /product= "LIPAM-10"
XX
PN   WO2003025150-A2.
XX
PD   27-MAR-2003.
XX
PF   19-SEP-2002; 2002WO-US029980.
XX
PR   21-SEP-2001; 2001US-0324039P.
PR   26-OCT-2001; 2001US-0346197P.
PR   02-NOV-2001; 2001US-0343876P.
PR   30-NOV-2001; 2001US-0334211P.
PR   14-DEC-2001; 2001US-0340223P.
PR   18-DEC-2001; 2001US-0342166P.
PR   22-JAN-2002; 2002US-0351262P.
PR   03-MAY-2002; 2002US-0377576P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Warren BA,  Emerling BM,  Lee EA,  Chang H,  Forsythe IJ,  Griffin JA;
PI   Baughn MR,  Chawla NK,  Khare R,  Reddy R,  Lee S,  Bulloch SA,  Lee SY;
PI   Tran UK,  Elliott VS,  Tang YT,  Bhatia U,  Burrill JD,  Blake JJ,  Ho A;
PI   Zheng W;
XX
DR   WPI; 2003-363142/34.
DR   P-PSDB; ABR43305.
XX
PT   New human lipid-associated molecules (LIPAM) useful for diagnosing,
PT   treating and preventing diseases or conditions associated with aberrant
PT   LIPAM expression, e.g. cancer, AIDS, atherosclerosis or infections.
XX
PS   Claim 5; Page 216-220; 225pp; English.
XX
CC   ACC49778 to ACC49794 encode the human lipid-associated molecule proteins
CC   given in ABR43296 to ABR43312, designated LIPAM-1 to LIPAM-17 (I). (I)
CC   have cytostatic, antiarteriosclerotic, anti-HIV, antiallergic, nootropic,
CC   cerebroprotective, antiparkinsonian, anticonvulsant, antiinflammatory,
CC   antiulcer, hepatotropic, antibacterial, virucide, protozoacide, cardiant,
CC   antiparasitic and antilipaemic activities, and can be used in gene
CC   therapy. The LIPAM polypeptides and polynucleotides are useful in
CC   diagnosing, treating and preventing diseases or conditions associated
CC   with decreased expression or overexpression of LIPAM, such as cell
CC   proliferative diseases (e.g. cancer or atherosclerosis), autoimmune/
CC   inflammatory diseases (e.g. AIDS or allergies), neurological disorders
CC   (e.g. stroke, Parkinson's disease or epilepsy), gastrointestinal (e.g.
CC   ulcer or cirrhosis), cardiovascular (e.g. myocardial infarction),
CC   metabolic (e.g. obesity), developmental, endocrine, or pulmonary
CC   disorders, infections (e.g. bacterial, viral, parasitic or protozoal),
CC   and disorders of lipid metabolism. They are also useful in assessing the
CC   effects of exogenous compounds on the expression of nucleic acid and
CC   amino acid sequences of LIPAM. The LIPAMs or their fragments are useful
CC   in screening compounds for effectiveness as agonist or antagonist of the
CC   polypeptides, or in altering the expression of the target polynucleotide
CC   and compounds that specifically bind to or modulate the activity of the
CC   polypeptide
XX
SQ   Sequence 13869 BP; 3589 A; 3879 C; 3551 G; 2850 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 144.4;  DB 10;  Length 13869;
  Best Local Similarity   89.5%;  Pred. No. 3.5e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13150 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 13209

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db      13210 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 13269

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||    |  ||| |  ||
Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321


RESULT 10
ACC47280
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ID   ACC47280 standard; DNA; 13938 BP.
XX
AC   ACC47280;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human apolipoprtein(a) encoding DNA.
XX
KW   Apolipoprotein(a); antiarteriosclerotic; cardiant; gene therapy; human;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             46. .13692
FT                   /*tag=  a
FT                   /product= "apolipoprotein(a)"
XX
PN   WO2003014307-A2.
XX
PD   20-FEB-2003.
XX
PF   05-AUG-2002; 2002WO-US024920.
XX
PR   07-AUG-2001; 2001US-00923515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-256565/25.
DR   P-PSDB; ABR39860.
XX
PT   New antisense compound, useful for preparing a composition for treating
PT   abnormal lipid or cholesterol metabolism, atherosclerosis or
PT   cardiovascular disease.
XX
PS   Example 13; Page 92-112; 120pp; English.
XX
CC   The invention relates to a new compound, 8-50 nucleobases in length
CC   targeted to a nucleic acid molecule encoding human apolipoprotein(a),
CC   specifically hybridizes with and inhibits the expression of human
CC   apolipoprotein(a). The antisense compounds are useful for preparing a
CC   composition for treating abnormal lipid or cholesterol metabolism,
CC   atherosclerosis or cardiovascular disease. The present sequence
CC   represents a DNA encoding the human apoliprotein(a) (GenBank accession
CC   No.NM_005577)
XX
SQ   Sequence 13938 BP; 3613 A; 3889 C; 3560 G; 2876 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 144.4;  DB 8;  Length 13938;
  Best Local Similarity   89.5%;  Pred. No. 3.5e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db      13150 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 13209

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db      13210 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 13269

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||||||||    |  ||| |  ||
Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321


RESULT 11
ADO33412
ID   ADO33412 standard; DNA; 13938 BP.
XX
AC   ADO33412;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human apolipoprotein(a) [Lp(a)] DNA - SEQ 860.
XX
KW   apolipoprotein B; ApoB; cardiovascular; antiarteriosclerotic;
KW   antilipaemic; antidiabetic; anorectic; cardiant; vasotropic; hypotensive;
KW   anabolic; eating disorder; cytostatic; endocrine; vasotropic;
KW   neuroprotective; nootropic; lipid; cholesterol metabolism;
KW   hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW   Von Gierke's disease; lipodystrophy; Cushing's syndrome;
KW   sexual ateliotic dwarfism; hyperthyroidism; hypertension;
KW   anorexia nervosa; Werner's syndrome; hepatoma; multiple myeloma; uraemia;
KW   impotence; obstructive liver disease; Alzheimer's; dementia; diabetes;
KW   obesity; atherosclerosis; human; ds; apolipoprotein(a); Lp(a).
XX
OS   Homo sapiens.
XX
PN   WO2004044181-A2.
XX
PD   27-MAY-2004.
XX
PF   13-NOV-2003; 2003WO-US036411.
XX
PR   13-NOV-2002; 2002US-0426234P.
PR   15-MAY-2003; 2003WO-US015493.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke R,  Graham M,  Lemonidis-Tarbet K,  Dobie KW;
XX
DR   WPI; 2004-420321/39.
XX
PT   Antisense oligonucleotide compound that inhibits expression of mRNA
PT   encoding human apolipoprotein B, useful for treating hyperlipidemia,
PT   diabetes, obesity, von Gierke's disease, lipodystrophies, Cushing's
PT   syndrome.
XX
PS   Example 57; SEQ ID NO 860; 483pp; English.
XX
CC   The invention relates to a novel antisense compound where the compound
CC   hybridises to and inhibits expression of mRNA encoding human
CC   apolipoprotein B (ApoB) after 16-24 hours by at least 30% in 80%
CC   confluent HepG2 cells in culture at a concentration of 150 nM. The
CC   compound of the invention demonstrates cardiovascular,
CC   antiarteriosclerotic, antilipaemic, antidiabetic, anorectic, cardiant,
CC   vasotropic, hypotensive, anabolic, eating disorder-related, cytostatic,
CC   endocrine, vasotropic, neuroprotective and nootropic activities and may
CC   be useful for inhibiting the expression of apolipoprotein B in cells or
CC   tissues in vivo in order to address a condition associated with abnormal
CC   lipid or cholesterol metabolism. The compound may be useful for
CC   decreasing circulating lipoprotein levels, triglyceride levels,
CC   cholesterol levels, lipid levels, fatty acid levels, acute phase
CC   reactants and chylomicrons and thus may be utilised during treatment of
CC   hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia,
CC   cardiovascular disorders, Von Gierke's disease, lipodystrophy, Cushing's
CC   syndrome, sexual ateliotic dwarfism, hyperthyroidism, hypertension,
CC   anorexia nervosa, Werner's syndrome, hepatoma, multiple myeloma, uraemia,
CC   impotence, obstructive liver disease, Alzheimer's disease, dementia,
CC   diabetes, obesity and atherosclerosis. The current sequence is that of
CC   the human apolipoprotein(a) [Lp(a)] DNA - SEQ ID 860 of the invention.
XX
SQ   Sequence 13938 BP; 3614 A; 3889 C; 3560 G; 2875 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 144.4;  DB 12;  Length 13938;
  Best Local Similarity   89.5%;  Pred. No. 3.5e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db      13150 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 13209

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
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Db      13210 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 13269

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||    |  ||| |  ||
Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321


RESULT 12
ADQ75139
ID   ADQ75139 standard; cDNA; 13938 BP.
XX
AC   ADQ75139;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human apolipoprotein A cDNA.
XX
KW   cardiovascular; antiarteriosclerotic; antilipemic; vasotropic;
KW   apolipoprotein modulator A; apolipoprotein A; plasminogen;
KW   apolipoprotein A associated disorder; cardiovascular disorder;
KW   atherosclerosis; hypercholesterolaemia; coronary artery disease; human;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2004138164-A1.
XX
PD   15-JUL-2004.
XX
PF   15-OCT-2003; 2003US-00684440.
XX
PR   07-AUG-2001; 2001US-00923515.
PR   02-JUN-2003; 2003US-0475402P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2004-533399/51.
DR   P-PSDB; ADQ75209.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating conditions with aberrant expression of
PT   apolipoprotein(a), such as atherosclerosis, hypercholesterolemia and
PT   coronary artery disease.
XX
PS   Example 13; SEQ ID NO 4; 54pp; English.
XX
CC   The invention describes a new compound (I) comprising 8-80 nucleobases in
CC   length targeted to a nucleic acid molecule encoding apolipoprotein(a),
CC   where the compound is at least 70% complementary to the nucleic acid
CC   molecule encoding apolipoprotein(a), and inhibits the expression of
CC   apolipoprotein(a) mRNA by at least 10%. Also described are: a method of
CC   inhibiting the expression of apolipoprotein(a) in cells or tissues; a
CC   method of treating an animal having a disease or condition associated
CC   with apolipoprotein(a); a method of screening for a modulator of
CC   apolipoprotein(a); a diagnostic method for identifying a disease state,
CC   comprising identifying the presence of apolipoprotein(a) in a sample
CC   using at least one of the primers selected from a fully defined sequence
CC   of 25, 18 or 24 bp (SEQ ID NO: 5, 6 or 7) as given in the specification;
CC   a kit or assay device comprising (I); and a method of inhibiting the
CC   expression of apolipoprotein(a), comprising contacting a biological
CC   system expressing human apolipoprotein(a) with a synthetic antisense
CC   compound, where the synthetic antisense compound comprises 15-30
CC   nucleobases in length and has at least 3 mismatches to human plasminogen.
CC   The methods and compositions of the present invention are useful for the
CC   diagnosis, prevention and/or treatment of diseases or conditions
CC   associated with aberrant expression or activity of apolipoprotein(a),
CC   such as cardiovascular disorder, atherosclerosis, hypercholesterolaemia,
CC   coronary artery disease and/or their combinations. This sequence encodes
CC   human apolipoprotein A.
XX
SQ   Sequence 13938 BP; 3613 A; 3889 C; 3560 G; 2876 T; 0 U; 0 Other;

  Query Match            72.0%;  Score 144.4;  DB 12;  Length 13938;
  Best Local Similarity  89.5%;  Pred. No. 3.5e-39;
  Matches  154;  Conservative    1;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||||||
Db      13150 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 13209

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db      13210 GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC 13269

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||    |  ||| |  ||
Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321


RESULT 13
ADQ38545
ID   ADQ38545 standard; DNA; 13938 BP.
XX
AC   ADQ38545;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 208.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
DR   P-PSDB; ADQ39373.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 208; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
```

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CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a human myocardial infarction-
CC   associated gene containing one or more SNP's of the invention. Note: This
CC   sequence was not shown in the specification. The sequence has come from
CC   an electronic sequence listing downloaded from the WIPO website.
XX
SQ   Sequence 13938 BP; 3611 A; 3880 C; 3553 G; 2873 T; 0 U; 21 Other;

  Query Match             72.0%;  Score 144.4;  DB 13;  Length 13938;
  Best Local Similarity   90.1%;  Pred. No. 3.5e-39;
  Matches  155;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          9 CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
              | |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db      13150 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 13209

Qy         69 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13210 GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 13269

Qy        129 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||    |  ||| |  ||
Db      13270 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 13321


RESULT 14
AAS80436/c
ID   AAS80436 standard; cDNA; 2178 BP.
XX
AC   AAS80436;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #16240.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG16249.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 1; SEQ ID NO 16240; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 2178 BP; 453 A; 532 C; 574 G; 619 T; 0 U; 0 Other;

  Query Match             66.2%;  Score 132.8;  DB 5;  Length 2178;
  Best Local Similarity   88.3%;  Pred. No. 1.7e-35;
  Matches  143;  Conservative    1;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         19 CTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAACC 78
              | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        272 CAAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAATC 213

Qy         79 TCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACACAAGCAG 138
              ||||| | ||||||||||||||:||||||||||||||||||||||||||||||| |  ||
Db        212 TCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCCACACGAAAAG 153

Qy        139 ATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||    |  ||| |  ||
Db        152 ATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 111


RESULT 15
ACH00783
ID   ACH00783 standard; DNA; 744 BP.
XX
AC   ACH00783;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human micro-plasminogen gene SEQ ID NO: 64.
XX
KW   Recombinant protein production; plasminogen; signal peptide;
KW   plasminogen activator identification; protease; wound healing; vulnerary;
KW   anticoagulant; thrombolytic; cardiant; cerebroprotective; vasotropic;
KW   antiinflammatory; ophthalmological; thrombosis; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003066842-A2.
XX
PD   14-AUG-2003.
XX
PF   06-FEB-2003; 2003WO-DE000341.
XX
PR   06-FEB-2002; 2002EP-00002716.
PR   21-FEB-2002; 2002US-0357809P.
XX
PA   (TROM-) TROMMSDORFF ARZNEIMITTEL GMBH & CO KG.
XX
PI   Susilo R,  Korting HC,  Gassen HG,  Hils M,  Pasternack R;
XX
DR   WPI; 2003-697451/66.
XX
PT   Recombinant production of plasminogen as a fusion protein comprising a
PT   signal peptide that can be removed by proteolysis is useful as an
PT   antithrombotic and anticoagulant.
XX
```

PS Claim 25; Page 68-69; 140pp; German.
XX
CC The present invention relates to a method of producing a recombinant
CC functional plasminogen in microorganisms. The method comprises a sequence
CC encoding at least a functional part of such a plasminogen and a sequence
CC encoding a signal peptide that are fused together, where the two
CC sequences are linked through codons that encode a protease cleavage site
CC to allow removal of the signal peptide. The plasminogen is used to screen
CC for plasminogen activators. Both plasminogen and plasmin, prepared from
CC it by activation, are used for treatment of wounds and the
CC treatment/prevention of thrombotic events, including use in wound
CC dressings, as antithrombotic and anticoagulant agents for preventing or
CC treating a wide variety of conditions, e.g. cardiac infarct, stroke,
CC thrombosis, restenosis, hypoxia, ischaemia, vascular inflammation,
CC pulmonary embolism, conjunctivitis (plasminogen type-I deficiency), burns
CC and disseminated intravascular coagulation. The present sequence is a
CC coding sequence used in the exemplification of the invention
XX
SQ Sequence 744 BP; 177 A; 169 C; 207 G; 191 T; 0 U; 0 Other;

Query Match 66.1%; Score 132.6; DB 10; Length 744;
Best Local Similarity 85.0%; Pred. No. 1.3e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

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Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db        174 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 233

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:||||||||||||||||||||||||||
Db        234 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 293

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||     |  ||| |  ||
Db        294 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 346
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Search completed: May 26, 2006, 14:14:02
Job time : 357 secs

GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 13:47:50 ; Search time 94 Seconds
(without alignments)
4000.988 Million cell updates/sec

Title: US-10-796-280-19350
Perfect score: 200.6
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	187.4	93.4	601	3	US-09-949-016-146441	Sequence 146441,
2	186.2	92.8	55195	3	US-09-949-016-15854	Sequence 15854, A
3	132.6	66.1	1724	10	5200340-5	Patent No. 5200340
4	132.6	66.1	1907	3	US-10-000-489-53	Sequence 53, Appl
5	132.6	66.1	1907	4	US-09-992-095B-53	Sequence 53, Appl
6	132.6	66.1	1907	5	US-10-000-986A-53	Sequence 53, Appl
7	132.6	66.1	2296	2	US-07-750-080A-18	Sequence 18, Appl
8	132.6	66.1	2296	3	US-08-651-472-18	Sequence 18, Appl
9	132.6	66.1	2296	3	US-08-358-928-18	Sequence 18, Appl
10	132.6	66.1	2430	3	US-09-192-012-4	Sequence 4, Appli
11	132.6	66.1	2497	2	US-08-643-219-12	Sequence 12, Appl
12	132.6	66.1	2497	2	US-09-131-995-12	Sequence 12, Appl
13	132.6	66.1	2497	2	US-08-832-087B-12	Sequence 12, Appl
14	132.6	66.1	2497	3	US-08-851-350-12	Sequence 12, Appl
15	132.6	66.1	2497	3	US-09-132-154-12	Sequence 12, Appl
16	132.6	66.1	2497	3	US-08-924-287A-12	Sequence 12, Appl
17	132.6	66.1	2497	5	US-09-946-893C-1	Sequence 1, Appli
18	132.6	66.1	2679	10	5200340-7	Patent No. 5200340
19	132.6	66.1	2732	3	US-09-949-016-4112	Sequence 4112, Ap
20	132.6	66.1	2753	2	US-07-854-603-1	Sequence 1, Appli
21	131	65.3	690	2	US-08-379-621-1	Sequence 1, Appli
22	131	65.3	690	2	US-08-889-078-1	Sequence 1, Appli
23	38.6	19.2	39	2	US-08-456-840-13	Sequence 13, Appl
24	38.6	19.2	39	2	US-08-266-407A-13	Sequence 13, Appl
25	38.6	19.2	39	2	US-08-892-544-13	Sequence 13, Appl
26	36	17.9	36	2	US-08-456-840-19	Sequence 19, Appl
27	36	17.9	36	2	US-08-456-840-21	Sequence 21, Appl
28	36	17.9	36	2	US-08-266-407A-19	Sequence 19, Appl
29	36	17.9	36	2	US-08-266-407A-21	Sequence 21, Appl
30	36	17.9	36	2	US-08-892-544-19	Sequence 19, Appl
31	36	17.9	36	2	US-08-892-544-21	Sequence 21, Appl
32	33	16.5	33	2	US-08-456-840-1	Sequence 1, Appli
33	33	16.5	33	2	US-08-266-407A-1	Sequence 1, Appli
34	33	16.5	33	2	US-08-892-544-1	Sequence 1, Appli
c 35	33	16.5	41863	3	US-09-949-016-14948	Sequence 14948, A
c 36	33	16.5	49440	3	US-09-949-016-14150	Sequence 14150, A
c 37	31.4	15.7	86380	3	US-09-949-016-14837	Sequence 14837, A
38	30.4	15.2	18554	3	US-09-811-825A-3	Sequence 3, Appli
39	30.4	15.2	18554	3	US-10-652-164-3	Sequence 3, Appli
40	30.4	15.2	32616	3	US-09-949-016-13407	Sequence 13407, A
c 41	30.2	15.1	147	3	US-09-513-999C-16218	Sequence 16218, A
c 42	29.4	14.7	456	3	US-09-621-976-141	Sequence 141, App
43	29	14.5	601	3	US-09-949-016-130514	Sequence 130514,
44	29	14.5	601	3	US-09-949-016-130515	Sequence 130515,
c 45	29	14.5	197875	3	US-09-949-016-15425	Sequence 15425, A

ALIGNMENTS

RESULT 1
US-09-949-016-146441
; Sequence 146441, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146441
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-146441

Query Match 93.4%; Score 187.4; DB 3; Length 601;
Best Local Similarity 95.0%; Pred. No. 4.9e-55;
Matches 191; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```
Qy       1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
          |||||:|||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db     296 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 355

Qy      61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
          |||||||||||||||| |||||| | ||||||||||||||:|||||||||||||||||||
Db     356 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 415

Qy     121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
          |||||||||||| | |||||||||||||||||||||||||||||||||| |||||||||
Db     416 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 475

Qy     181 GTCTTCACCCCACGCTGGTGA 201
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Db     476 GTCTTCACCCCACGCTGGTGA 496
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RESULT 2
US-09-949-016-15854
; Sequence 15854, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15854
;   LENGTH: 55195
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15854

  Query Match             92.8%;  Score 186.2;  DB 3;  Length 55195;
  Best Local Similarity   95.0%;  Pred. No. 9.3e-54;
  Matches  191;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              ||||| |||||||||||||||||| |||||||||||||||||||||||||||||||||
Db      38902 TTGACGTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 38961

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | ||||||||||||||:||||||||||||||||||
Db      38962 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 39021

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||||| |||||||||
Db      39022 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 39081

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      39082 GTCTTCACCCCACGCTGGTGA 39102


RESULT 3
5200340-5
;Patent No. 5200340
;     APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
;PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
;     TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
;ACTIVATORS
;     NUMBER OF SEQUENCES: 34
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/53,412
;       FILING DATE: 22-MAY-1987
;SEQ ID NO:5:
;       LENGTH: 1724
5200340-5

  Query Match             66.1%;  Score 132.6;  DB 10;  Length 1724;
  Best Local Similarity   85.0%;  Pred. No. 8.9e-36;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db       1086 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1145

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:||||||||||||||||||||||||||
Db       1146 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1205

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db       1206 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1258


RESULT 4
US-10-000-489-53
; Sequence 53, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US6.DIV
;  CURRENT APPLICATION NUMBER: US/10/000,489
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: JPatent
; SEQ ID NO 53
;   LENGTH: 1907
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..1043
;   NAME/KEY: CDS
;   LOCATION: 1044..1664
;   NAME/KEY: 3'UTR
;   LOCATION: 1665..1907
;   NAME/KEY: polyA_signal
;   LOCATION: 1869..1874
;   NAME/KEY: polyA_site
;   LOCATION: 1892..1907
US-10-000-489-53

  Query Match             66.1%;  Score 132.6;  DB 3;  Length 1907;
  Best Local Similarity   85.0%;  Pred. No. 9.3e-36;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db       1097 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1156

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:||||||||||||||||||||||||||
Db       1157 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1216

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db       1217 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1269


RESULT 5
US-09-992-095B-53
; Sequence 53, Application US/09992095B
; Patent No. 6989262
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US5.DIV
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;  CURRENT APPLICATION NUMBER: US/09/992,095B
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: JPatent
; SEQ ID NO 53
;    LENGTH: 1907
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: 5'UTR
;    LOCATION: 1..1043
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 1044..1664
;    FEATURE:
;    NAME/KEY: 3'UTR
;    LOCATION: 1665..1907
;    FEATURE:
;    NAME/KEY: polyA_signal
;    LOCATION: 1869..1874
;    FEATURE:
;    NAME/KEY: polyA_site
;    LOCATION: 1892..1907
US-09-992-095B-53

  Query Match             66.1%;  Score 132.6;  DB 4;  Length 1907;
  Best Local Similarity   85.0%;  Pred. No. 9.3e-36;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db       1097 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1156

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db       1157 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1216

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||     |  |||  |  ||
Db       1217 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1269


RESULT 6
US-10-000-986A-53
; Sequence 53, Application US/10000986A
; Patent No. 7005500
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: G-091US09DIV
;  CURRENT APPLICATION NUMBER: US/10/000,986A
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: JPatent
; SEQ ID NO 53
;    LENGTH: 1907
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: 5'UTR
;    LOCATION: 1..1043
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 1044..1664
;    FEATURE:
;    NAME/KEY: 3'UTR
;    LOCATION: 1665..1907
;    FEATURE:
;    NAME/KEY: polyA_signal
;    LOCATION: 1869..1874
;    FEATURE:
;    NAME/KEY: polyA_site
;    LOCATION: 1892..1907
US-10-000-986A-53

  Query Match             66.1%;  Score 132.6;  DB 5;  Length 1907;
  Best Local Similarity   85.0%;  Pred. No. 9.3e-36;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db       1097 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1156

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db       1157 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1216

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||     |  |||  |  ||
Db       1217 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1269


RESULT 7
US-07-750-080A-18
; Sequence 18, Application US/07750080A
; Patent No. 5445953
; GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  DIRECT MOLECULAR CLONING OF A MODIFIED
;    TITLE OF INVENTION:  EUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/750,080A
;      FILING DATE:  19910826
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
```

```
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/106 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2296 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  pN2gpt-LPg (Fig. 5.3)
US-07-750-080A-18

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 2296;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db       1652 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1711

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db       1712 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1771

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||||     |  ||| |  ||
Db       1772 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1824


RESULT 8
US-08-651-472-18
; Sequence 18, Application US/08651472
; Patent No. 6103244
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, Friedrich
;    APPLICANT:  SCHEIFLINGER, Friedrich
;    APPLICANT:  FALKNER, Falko Gunter
;    APPLICANT:  PFLEIDERER, Michael
;    TITLE OF INVENTION:  DIRECT MOLECULAR CLONING OF CHIMERIC
;    TITLE OF INVENTION:  VIRUSES CONTAINING HUMAN IMMUNODEFCIENCY VIRUS TYPE 1
;    TITLE OF INVENTION:  (HIV-1) ANTIGENS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/651,472
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/914,738
;      FILING DATE:  20-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/750,080
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/166/IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2296 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
;    IMMEDIATE SOURCE:
;      CLONE:  pN2gpt-LPg
US-08-651-472-18

  Query Match             66.1%;  Score 132.6;  DB 3;  Length 2296;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db       1652 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1711

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:|||||||||||||||||||||||||||
Db       1712 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1771

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||||     |  ||| |  ||
Db       1772 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1824


RESULT 9
US-08-358-928-18
; Sequence 18, Application US/08358928
; Patent No. 6265183
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, Friedrich
;    APPLICANT:  SCHEIFLINGER, Friedrich
;    APPLICANT:  FALKNER, Falko Gunter
;    APPLICANT:  PFLEIDERER, Michael
;    TITLE OF INVENTION:  DIRECT MOLECULAR CLONING OF CHIMERIC
;    TITLE OF INVENTION:  VIRUSES CONTAINING HUMAN IMMUNODEFCIENCY VIRUS TYPE 1
;    TITLE OF INVENTION:  (HIV-1) ANTIGENS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358;928
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/914,738
;      FILING DATE:  20-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/750,080
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/166/IMMU
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2296 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  Other nucleic acid;
;       DESCRIPTION:  Synthetic DNA oligonucleotide
;     IMMEDIATE SOURCE:
;       CLONE:  pN2gpt-LPg
US-08-358-928-18

  Query Match             66.1%;  Score 132.6;  DB 3;  Length 2296;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||||
Db       1652 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1711

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db       1712 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1771

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db       1772 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 1824


RESULT 10
US-09-192-012-4
; Sequence 4, Application US/09192012A
; Patent No. 6475784
; GENERAL INFORMATION:
;  APPLICANT: Papkoff, Jackie
;  APPLICANT: Megabios Corporation
;  APPLICANT: Pfizer, Inc.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Delivery of Nucleic Acids
;  TITLE OF INVENTION: Encoding Anti-Angiogenis Polypeptides
;  FILE REFERENCE: 018484-000110US
;  CURRENT APPLICATION NUMBER: US/09/192,012A
;  CURRENT FILING DATE: 1998-11-13
;  EARLIER APPLICATION NUMBER: US 60/066,020
;  EARLIER FILING DATE: 1997-11-14
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2430
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2430)
;   OTHER INFORMATION: human plasminogen
US-09-192-012-4

  Query Match             66.1%;  Score 132.6;  DB 3;  Length 2430;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||||
Db       1863 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1922

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db       1923 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 1982

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db       1983 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2035


RESULT 11
US-08-643-219-12
; Sequence 12, Application US/08643219
; Patent No. 5801146
;  GENERAL INFORMATION:
;    APPLICANT:  Davidson, Donald J.
;    TITLE OF INVENTION:  NOVEL ANTIANGIOGENIC PEPTIDES
;    TITLE OF INVENTION:  AND METHODS FOR INHIBITING ANGIOGENESIS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/643,219
;      FILING DATE:  06-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Casuto, Dianne
;      REGISTRATION NUMBER:  40,943
;      REFERENCE/DOCKET NUMBER:  5940.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847-938-3137
;      TELEFAX:  847-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2497 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-643-219-12

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 2497;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||||
Db       1912 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1971

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db       1972 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2031

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||||     |  ||| |  ||
Db       2032 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2084


RESULT 12
US-09-131-995-12
; Sequence 12, Application US/09131995
; Patent No. 5972896
;  GENERAL INFORMATION:
;    APPLICANT:  Davidson, Donald J.
;    TITLE OF INVENTION:  NOVEL ANTIANGIOGENIC PEPTIDES
;    TITLE OF INVENTION:  AND METHODS FOR INHIBITING ANGIOGENESIS
```

```
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/131,995
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,087
;      FILING DATE:  03-APR-1997
;      APPLICATION NUMBER:  08/643,219
;      FILING DATE:  06-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Casuto, Dianne
;      REGISTRATION NUMBER:  40,943
;      REFERENCE/DOCKET NUMBER:  5940.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847-938-3137
;      TELEFAX:  847-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2497 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-131-995-12

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 2497;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db       1912 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1971

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:||||||||||||||||||||||||||
Db       1972 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2031

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  | |||||||||||||||||||||||||||      |  ||| |  ||
Db       2032 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2084


RESULT 13
US-08-832-087B-12
; Sequence 12, Application US/08832087B
; Patent No. 5981484
;  GENERAL INFORMATION:
;    APPLICANT:  Davidson, Donald J.
;    TITLE OF INVENTION:  NOVEL ANTIANGIOGENIC PEPTIDES
;    TITLE OF INVENTION:  AND METHODS FOR INHIBITING ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,087B
;      FILING DATE:  03-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/643,219
;      FILING DATE:  06-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Casuto, Dianne
;      REGISTRATION NUMBER:  40,943
;      REFERENCE/DOCKET NUMBER:  5940.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847-938-3137
;      TELEFAX:  847-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2497 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-832-087B-12

  Query Match             66.1%;  Score 132.6;  DB 2;  Length 2497;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db      .1912 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1971

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | |||||||||||||:||||||||||||||||||||||||||
Db       1972 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2031

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  | |||||||||||||||||||||||||||      |  ||| |  ||
Db       2032 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2084


RESULT 14
US-08-851-350-12
; Sequence 12, Application US/08851350
; Patent No. 6057122
;  GENERAL INFORMATION:
;    APPLICANT:  Abbott Laboratories
;    TITLE OF INVENTION:  NOVEL ANTIANGIOGENIC PEPTIDES,
;    TITLE OF INVENTION:  POLYNUCLEOTIDES ENCODING SAME AND METHODS
;    TITLE OF INVENTION:  FOR INHIBITING ANGIOGENESIS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/851,350
;      FILING DATE:  05-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Casuto, Dianne
;      REGISTRATION NUMBER:  40,943
;      REFERENCE/DOCKET NUMBER:  5940.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847-938-3137
;      TELEFAX:  847-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2497 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-851-350-12

  Query Match             66.1%;  Score 132.6;  DB 3;  Length 2497;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db       1912 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1971

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
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Db       1972 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2031

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||||      |  ||| |  ||
Db       2032 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2084


RESULT 15
US-09-132-154-12
; Sequence 12, Application US/09132154
; Patent No. 6251867
;  GENERAL INFORMATION:
;    APPLICANT:  Davidson, Donald J.
;    TITLE OF INVENTION:  NOVEL ANTIANGIOGENIC PEPTIDES
;    TITLE OF INVENTION:  AND METHODS FOR INHIBITING ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/132,154
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,087
;      FILING DATE:  03-APR-1997
;      APPLICATION NUMBER:  08/643,219
;      FILING DATE:  06-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Casuto, Dianne
;      REGISTRATION NUMBER:  40,943
;      REFERENCE/DOCKET NUMBER:  5940.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847-938-3137
;      TELEFAX:  847-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2497 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-132-154-12

  Query Match             66.1%;  Score 132.6;  DB 3;  Length 2497;
  Best Local Similarity   85.0%;  Pred. No. 1e-35;
  Matches  147;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||||
Db       1912 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1971

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:|||||||||||||||||||||||||
Db       1972 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2031

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||| |  |||||||||||||||||||||||||||      |  ||| |  ||
Db       2032 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2084


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Job time : 96 secs
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GenCore version 5.1.8

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Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	200.6	100.0	201	9	US-10-741-600-28344	Sequence 28344, A
	2	200.6	100.0	201	10	US-10-995-561-25501	Sequence 25501, A
c	3	200.6	100.0	201	15	US-11-124-368A-8354	Sequence 8354, Ap
	4	200.6	100.0	93112	9	US-10-741-600-17618	Sequence 17618, A
	5	200.6	100.0	93112	10	US-10-995-561-13234	Sequence 13234, A
c	6	187.4	93.4	614	4	US-09-925-065A-869309	Sequence 869309,
c	7	187.4	93.4	614	4	US-09-925-065A-886262	Sequence 886262,
c	8	187.4	93.4	614	5	US-09-925-065A-869309	Sequence 869309,
c	9	187.4	93.4	614	5	US-09-925-065A-886262	Sequence 886262,
	10	187.4	93.4	63693	8	US-10-741-601-5650	Sequence 5650, Ap
	11	187.4	93.4	63693	10	US-10-995-561-13269	Sequence 13269, A
	12	186.2	92.8	52280	16	US-11-108-459-9	Sequence 9, Appli
	13	172.8	86.1	201	8	US-10-741-601-14344	Sequence 14344, A
	14	172.8	86.1	201	10	US-10-995-561-34498	Sequence 34498, A
	15	164.6	82.1	91561	15	US-11-124-368A-2896	Sequence 2896, Ap
	16	144.4	72.0	201	9	US-10-741-600-6797	Sequence 6797, Ap
	17	144.4	72.0	201	9	US-10-741-600-6815	Sequence 6815, Ap
	18	144.4	72.0	201	10	US-10-995-561-4271	Sequence 4271, Ap
	19	144.4	72.0	201	15	US-11-124-368A-973	Sequence 973, App
	20	144.4	72.0	820	10	US-10-450-763-1915	Sequence 1915, Ap
	21	144.4	72.0	820	10	US-10-450-763-16241	Sequence 16241, A
	22	144.4	72.0	1400	10	US-10-956-157-6673	Sequence 6673, Ap
	23	144.4	72.0	3756	9	US-10-741-600-207	Sequence 207, App
	24	144.4	72.0	3756	10	US-10-995-561-92	Sequence 92, Appl
	25	144.4	72.0	3756	15	US-11-124-368A-59	Sequence 59, Appl
	26	144.4	72.0	10422	3	US-09-870-759-125	Sequence 125, App
	27	144.4	72.0	10422	3	US-09-751-708A-125	Sequence 125, App
	28	144.4	72.0	10422	9	US-10-428-817A-121	Sequence 121, App
	29	144.4	72.0	10422	10	US-10-937-758A-102	Sequence 102, App
	30	144.4	72.0	13938	3	US-09-923-515-3	Sequence 3, Appli
	31	144.4	72.0	13938	8	US-10-684-440-4	Sequence 4, Appli
	32	144.4	72.0	13938	9	US-10-712-795-860	Sequence 860, App
	33	144.4	72.0	13938	9	US-10-485-113-3	Sequence 3, Appli
	34	144.4	72.0	13938	9	US-10-920-612-860	Sequence 860, App
	35	144.4	72.0	13938	9	US-10-741-600-208	Sequence 208, App
	36	144.4	72.0	13938	10	US-10-956-157-1438	Sequence 1438, Ap
c	37	132.8	66.2	2178	10	US-10-450-763-16240	Sequence 16240, A
	38	132.6	66.1	201	8	US-10-741-601-2633	Sequence 2633, Ap
	39	132.6	66.1	201	10	US-10-995-561-7453	Sequence 7453, Ap
	40	132.6	66.1	744	10	US-10-503-910-64	Sequence 64, Appl
	41	132.6	66.1	750	8	US-10-450-976-3	Sequence 3, Appli
	42	132.6	66.1	750	10	US-10-729-475-3	Sequence 3, Appli
	43	132.6	66.1	750	10	US-10-503-910-63	Sequence 63, Appl
	44	132.6	66.1	783	10	US-10-503-910-62	Sequence 62, Appl
	45	132.6	66.1	786	10	US-10-503-910-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-741-600-28344
; Sequence 28344, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28344
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-28344

Query Match 100.0%; Score 200.6; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.5e-61;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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Db         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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Db        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180

Qy        181 GTCTTCACCCCACGCTGGTGA 201
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Db        181 GTCTTCACCCCACGCTGGTGA 201
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RESULT 2
US-10-995-561-25501
; Sequence 25501, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25501
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-25501

  Query Match            100.0%;  Score 200.6;  DB 10;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-61;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Db          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180

Qy        181 GTCTTCACCCCACGCTGGTGA 201
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Db        181 GTCTTCACCCCACGCTGGTGA 201


RESULT 3
US-11-124-368A-8354/c
; Sequence 8354, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  James J. Devlin
;  APPLICANT:  May Luke
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Vascular Diseases, Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001524
;  CURRENT APPLICATION NUMBER: US/11/124,368A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,845
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/625,936
;  PRIOR FILING DATE: 2004-11-09
;  NUMBER OF SEQ ID NOS: 21112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8354
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-124-368A-8354

  Query Match            100.0%;  Score 200.6;  DB 15;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-61;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
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Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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Db         81 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 22

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db         21 GTCTTCACCCCACGCTGGTGA 1


RESULT 4
US-10-741-600-17618
; Sequence 17618, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17618
;   LENGTH: 93112
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(93112)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
US-10-741-600-17618

  Query Match            100.0%;  Score 200.6;  DB 9;  Length 93112;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-60;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78990 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 79049

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79050 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 79109

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79110 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 79169

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      79170 GTCTTCACCCCACGCTGGTGA 79190


RESULT 5
US-10-995-561-13234
; Sequence 13234, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13234
```

```
;   LENGTH: 93112
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(93112)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13234

  Query Match             100.0%;  Score 200.6;  DB 10;  Length 93112;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-60;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78990 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 79049

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79050 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 79109

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79110 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 79169

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      79170 GTCTTCACCCCACGCTGGTGA 79190


RESULT 6
US-09-925-065A-869309/c
; Sequence 869309, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 869309
;   LENGTH: 614
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-869309

  Query Match             93.4%;  Score 187.4;  DB 4;  Length 614;
  Best Local Similarity   95.0%;  Pred. No. 3.8e-56;
  Matches  191;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||:|||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        406 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 347

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | ||||||||||||||:|||||||||||||||||||
Db        346 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 287

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||||||| |||||||||
Db        286 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 227

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db        226 GTCTTCACCCCACGCTGGTGA 206


RESULT 7
US-09-925-065A-886262/c
; Sequence 886262, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 886262
;   LENGTH: 614
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-886262

  Query Match             93.4%;  Score 187.4;  DB 4;  Length 614;
  Best Local Similarity   95.0%;  Pred. No. 3.8e-56;
  Matches  191;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||:|||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        406 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 347

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | ||||||||||||||:|||||||||||||||||||
Db        346 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 287

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||||||| |||||||||
Db        286 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 227

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db        226 GTCTTCACCCCACGCTGGTGA 206


RESULT 8
US-09-925-065A-869309/c
; Sequence 869309, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
```

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;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 869309
;   LENGTH: 614
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-869309

  Query Match             93.4%;  Score 187.4;  DB 5;  Length 614;
  Best Local Similarity   95.0%;  Pred. No. 3.8e-56;
  Matches  191;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||:|||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        406 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 347

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:||||||||||||||||||||
Db        346 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 287

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db        286 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 227

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db        226 GTCTTCACCCCACGCTGGTGA 206


RESULT 9
US-09-925-065A-886262/c
; Sequence 886262, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 886262
;   LENGTH: 614
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-886262

  Query Match             93.4%;  Score 187.4;  DB 5;  Length 614;
  Best Local Similarity   95.0%;  Pred. No. 3.8e-56;
  Matches  191;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||:|||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        406 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 347

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:||||||||||||||||||||

Db        346 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 287

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db        286 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 227

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db        226 GTCTTCACCCCACGCTGGTGA 206


RESULT 10
US-10-741-601-5650
; Sequence 5650, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5650
;   LENGTH: 63693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5650

  Query Match             93.4%;  Score 187.4;  DB 8;  Length 63693;
  Best Local Similarity   95.0%;  Pred. No. 2.6e-55;
  Matches  191;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||:|||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      42930 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 42989

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:||||||||||||||||||||
Db      42990 CACACCAAGAAGTGAATCTCGAACCRCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 43049

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db      43050 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 43109

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      43110 GTCTTCACCCCACGCTGGTGA 43130


RESULT 11
US-10-995-561-13269
; Sequence 13269, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13269
;   LENGTH: 63693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13269

  Query Match             93.4%;  Score 187.4;  DB 10;  Length 63693;
  Best Local Similarity   95.0%;  Pred. No. 2.6e-55;
```

```
  Matches  191;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||:|||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      42930 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 42989

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:|||||||||||||||||||
Db      42990 CACACCAAGAAGTGAATCTCGAACCRCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 43049

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db      43050 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 43109

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      43110 GTCTTCACCCCACGCTGGTGA 43130


RESULT 12
US-11-108-459-9
; Sequence 9, Application US/11108459
; Publication No. US20060051780A1
; GENERAL INFORMATION:
;  APPLICANT: Zaas, Aimee
;  APPLICANT:  Schwartz, David A.
;  APPLICANT:  Peltz, Gary
;  TITLE OF INVENTION: Polymorphic Plasminogen Genes and Uses Thereof
;  FILE REFERENCE: DUKE-09785
;  CURRENT APPLICATION NUMBER: US/11/108,459
;  CURRENT FILING DATE:  2005-04-18
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 52280
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-108-459-9

  Query Match             92.8%;  Score 186.2;  DB 16;  Length 52280;
  Best Local Similarity   95.0%;  Pred. No. 6.4e-55;
  Matches  191;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      37409 TTGACGTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 37468

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:|||||||||||||||||||
Db      37469 CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 37528

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db      37529 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 37588

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||
Db      37589 GTCTTCACCCCACGCTGGTGA 37609


RESULT 13
US-10-741-601-14344
; Sequence 14344, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14344
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-14344

  Query Match             86.1%;  Score 172.8;  DB 8;  Length 201;
  Best Local Similarity   95.2%;  Pred. No. 4.2e-51;
  Matches  177;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         16 TTGACATCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 75

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:|||||||||||||||||||
Db         76 CACACCAAGAAGTGAATCTCGAACCRCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 135

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db        136 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 195

Qy        181 GTCTTC 186
              ||||||
Db        196 GTCTTC 201


RESULT 14
US-10-995-561-34498
; Sequence 34498, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-34498

  Query Match             86.1%;  Score 172.8;  DB 10;  Length 201;
  Best Local Similarity   95.2%;  Pred. No. 4.2e-51;
  Matches  177;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         16 TTGACATCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 75

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||| |||||| | |||||||||||||:|||||||||||||||||||
Db         76 CACACCAAGAAGTGAATCTCGAACCRCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 135

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||| |  |||||||||||||||||||||||||||||||| |||||||||
Db        136 TGGAGCCCACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG 195

Qy        181 GTCTTC 186
              ||||||
Db        196 GTCTTC 201


RESULT 15
US-11-124-368A-2896
; Sequence 2896, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Michele Cargill
;  APPLICANT:  James J. Devlin
;  APPLICANT:  May Luke
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Vascular Diseases, Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001524
;  CURRENT APPLICATION NUMBER: US/11/124,368A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,845
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/625,936
;  PRIOR FILING DATE: 2004-11-09
;  NUMBER OF SEQ ID NOS: 21112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2896
;   LENGTH: 91561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,
;   LOCATION: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31,
;   LOCATION: 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45,
;   LOCATION: 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59,
;   LOCATION: 60
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
;   LOCATION: 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89,
;   LOCATION: 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103,
;   LOCATION: 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126,
;   LOCATION: 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138,
;   LOCATION: 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150,
;   LOCATION: 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173,
;   LOCATION: 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185,
;   LOCATION: 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197,
;   LOCATION: 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220,
;   LOCATION: 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232,
;   LOCATION: 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244,
;   LOCATION: 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267,
;   LOCATION: 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279,
;   LOCATION: 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291,
;   LOCATION: 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302
;   OTHER INFORMATION: n = A,T,C or G
US-11-124-368A-2896

  Query Match             82.1%;  Score 164.6;  DB 15;  Length 91561;
  Best Local Similarity   98.0%;  Pred. No. 4.5e-47;
  Matches  197;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    3;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      77676 TTGACATCCTCATCTTTTCTAGGTCCTC-AGGCCTTCATCCTACAAGGTCATCCTGGGTG 77734

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |||||||||||||||||||||||||||| ||||||||||:||||||||||||||||||||

Db      77735 CACACCAAGAAGTGAACCTCGAATCTCA-GTTCAGGAAATAGAAGTGTCTAGGCTGTTCT 77793

Qy        121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||

Db      77794 TGGAGCCCACACAAGCAGATATTGCCTT-CTAAAGCTAAGCAGGTACTCGCTCACCTGTG 77852

Qy        181 GTCTTCACCCCACGCTGGTGA 201
              |||||||||||||||||||||

Db      77853 GTCTTCACCCCACGCTGGTGA 77873


Search completed: May 26, 2006, 14:28:23
Job time : 855 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 14:14:16 ; Search time 23 Seconds
(without alignments)
986.511 Million cell updates/sec

Title: US-10-796-280-19350
Perfect score: 200.6
Sequence: 1 ttgacatcctcatcttttct.....tcttcaccccacgctggtga 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	132.6	66.1	2732	6	US-10-473-173-75	Sequence 75, Appl
	2	30	15.0	889	6	US-10-953-349-15327	Sequence 15327, A
	3	27.8	13.9	3038	7	US-11-293-697-471	Sequence 471, App
c	4	27.6	13.8	393	6	US-10-953-349-11978	Sequence 11978, A
c	5	27.6	13.8	1057	6	US-10-953-349-19516	Sequence 19516, A
c	6	26.6	13.3	394191	6	US-10-506-549-3	Sequence 3, Appli
	7	26.4	13.2	1068	6	US-10-953-349-15193	Sequence 15193, A
	8	26.4	13.2	3420	6	US-10-953-349-9738	Sequence 9738, Ap
c	9	26.4	13.2	6050	6	US-10-511-937-2815	Sequence 2815, Ap
c	10	26.2	13.1	3059	7	US-11-293-697-1913	Sequence 1913, Ap
	11	25.4	12.7	1008	7	US-11-217-529-79011	Sequence 79011, A
c	12	25.2	12.6	1734	7	US-11-217-529-76402	Sequence 76402, A
c	13	25.2	12.6	2638	7	US-11-293-697-740	Sequence 740, App
c	14	25	12.5	631	6	US-10-488-619-2493	Sequence 2493, Ap
	15	25	12.5	4908	6	US-10-505-928-226	Sequence 226, App
	16	24.8	12.4	525	7	US-11-217-529-76870	Sequence 76870, A
	17	24.8	12.4	698	6	US-10-488-619-1977	Sequence 1977, Ap
	18	24.8	12.4	1537	6	US-10-501-834-212	Sequence 212, App
	19	24.8	12.4	3216	7	US-11-217-529-77601	Sequence 77601, A
	20	24.6	12.3	791	6	US-10-953-349-21923	Sequence 21923, A
c	21	24.6	12.3	1670	6	US-10-953-349-11818	Sequence 11818, A
c	22	24.6	12.3	1910	7	US-11-293-697-1893	Sequence 1893, Ap
	23	24.6	12.3	2108	6	US-10-505-928-856	Sequence 856, App
	24	24.6	12.3	2163	7	US-11-217-529-3294	Sequence 3294, Ap
	25	24.6	12.3	2254	7	US-11-293-697-286	Sequence 286, App
	26	24.6	12.3	3255	7	US-11-217-529-1043	Sequence 1043, Ap
c	27	24.6	12.3	3453	7	US-11-293-697-641	Sequence 641, App
	28	24.6	12.3	4894	6	US-10-511-937-566	Sequence 566, App
c	29	24.4	12.2	432	6	US-10-488-619-309	Sequence 309, App
c	30	24.4	12.2	709	6	US-10-953-349-39773	Sequence 39773, A
c	31	24.4	12.2	851	6	US-10-953-349-31	Sequence 31, Appl
	32	24.4	12.2	961	6	US-10-953-349-39485	Sequence 39485, A
c	33	24.4	12.2	1645	6	US-10-953-349-939	Sequence 939, App
c	34	24.4	12.2	2887	7	US-11-293-697-942	Sequence 942, App
	35	24.4	12.2	3871	6	US-10-196-749-347	Sequence 347, App
c	36	24.4	12.2	5262	7	US-11-217-529-786	Sequence 786, App
	37	24.2	12.1	988	6	US-10-953-349-4870	Sequence 4870, Ap
	38	24.2	12.1	1667	6	US-10-953-349-2736	Sequence 2736, Ap
c	39	24.2	12.1	1822	6	US-10-953-349-26846	Sequence 26846, A
	40	24.2	12.1	2113	6	US-10-953-349-11275	Sequence 11275, A
c	41	24.2	12.1	2763	6	US-10-953-349-9734	Sequence 9734, Ap
	42	24.2	12.1	128361	6	US-10-505-928-151	Sequence 151, App
	43	24	12.0	528	7	US-11-217-529-173718	Sequence 173718,
	44	24	12.0	669	6	US-10-473-173-296	Sequence 296, App
	45	24	12.0	669	6	US-10-473-173-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-473-173-75
; Sequence 75, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-75

Query Match 66.1%; Score 132.6; DB 6; Length 2732;
Best Local Similarity 85.0%; Pred. No. 2e-36;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

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Qy          8 CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
              || |  |||    | |||| ||||||||||||||||||||||||||||||||||||||
Db       1917 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1976

Qy         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
              ||||||||| |||||| | ||||||||||||||:||||||||||||||||||||||||||
Db       1977 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 2036

Qy        128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
              |||||  |  |||||||||||||||||||||||||||||     |  |||  |  ||
Db       2037 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2089
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RESULT 2
US-10-953-349-15327
; Sequence 15327, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

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;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15327
;    LENGTH: 889
;    TYPE: DNA
;    ORGANISM: Glycine max
US-10-953-349-15327

  Query Match             15.0%;  Score 30;  DB 6;  Length 889;
  Best Local Similarity   53.6%;  Pred. No. 0.27;
  Matches   60;  Conservative    1;  Mismatches   51;  Indels    0;  Gaps    0;

Qy         49 TCATCCTGGGTGCACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGT 108
              |||||    | |||||   ||| |  || || ||||  ||| ||    | ||:|||| ||
Db        694 TCATCACCTGAGCACAGGGAGAGGGAAATCTAGAATTACATTTTTCAAACATAGAAGAGT 753

Qy        109 CTAGGCTGTTCTTGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAG 160
              ||  |||| |    |   |      ||| | ||| | |  |  | |  ||
Db        754 GAAGCTTGTTTTGATTGAATATTTGTTCAGTTGTTGTCATTATTTATCATAG 805


RESULT 3
US-11-293-697-471
; Sequence 471, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 471
;    LENGTH: 3038
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-293-697-471

  Query Match             13.9%;  Score 27.8;  DB 7;  Length 3038;
  Best Local Similarity   50.4%;  Pred. No. 2.6;
  Matches   65;  Conservative    1;  Mismatches   63;  Indels    0;  Gaps    0;

Qy         34 CTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAACCTCGAATCTCATGTTC 93
              || ||||   ||  | |      ||| |  || ||  |||    |   | | | |||  |
Db        504 CTACATCTACCATTGGCCCAGAGGGGGTCCATCAGAAAGGAGTCAAAGTCTATGATGATG 563

Qy         94 AGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACACAAGCAGATATTGCCTTGCTAA 153
                | :| ||||| |  | ||  ||  |    |||   || ||| | ||   |||  |
Db        564 GTACCAAAGTAGTGTATGAGGTGCGCTCAGGAGGCACCGTAGTAGAAAATGGAGTGCACA 623

Qy        154 AGCTAAGCA 162
              |  ||||||
Db        624 AATTAAGCA 632


RESULT 4
US-10-953-349-11978/c
; Sequence 11978, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11978
;    LENGTH: 393
;    TYPE: DNA
;    ORGANISM: Glycine max
US-10-953-349-11978

  Query Match             13.8%;  Score 27.6;  DB 6;  Length 393;
  Best Local Similarity   52.8%;  Pred. No. 1.3;
  Matches   57;  Conservative    1;  Mismatches   50;  Indels    0;  Gaps    0;

Qy         26 CTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAACCTCGAATC 85
              | |||||   | ||| | | | || |   || |||    ||||         ||  |
Db        144 CACAAGGAAATAATCTTCCTATGTGAATGTGAGTGATGTCCAATCGAAACTACTTCATGA 85

Qy         86 TCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACACA 133
              ||||| ||| |||| :| || ||| || ||  |  |  |  |   |||
Db         84 TCATGATCATGAAAAAGTAGGGTCAAGACTCCTACTAAACACAGAACA 37


RESULT 5
US-10-953-349-19516/c
; Sequence 19516, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19516
;    LENGTH: 1057
;    TYPE: DNA
;    ORGANISM: Glycine max
US-10-953-349-19516

  Query Match             13.8%;  Score 27.6;  DB 6;  Length 1057;
  Best Local Similarity   52.8%;  Pred. No. 1.9;
  Matches   57;  Conservative    1;  Mismatches   50;  Indels    0;  Gaps    0;

Qy         26 CTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAACCTCGAATC 85
              | |||||   | ||| | | | || |   || |||    ||||         ||  |
Db        799 CACAAGGAAATAATCTTCCTATGTGAATGTGAGTGATGTCCAATCGAAACTACTTCATGA 740

Qy         86 TCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACACA 133
              ||||| ||| |||| :| || ||| || ||  |  |  |  |   |||
Db        739 TCATGATCATGAAAAAGTAGGGTCAAGACTCCTACTAAACACAGAACA 692


RESULT 6
US-10-506-549-3/c
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
;  APPLICANT: APPLERA CORPORATION
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL001361-US
;  CURRENT APPLICATION NUMBER: US/10/506,549
;  CURRENT FILING DATE:  2004-09-03
;  PRIOR APPLICATION NUMBER: 60/361,343
;  PRIOR FILING DATE: 2002-03-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;    LENGTH: 394191
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(394191)
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;   OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

  Query Match             13.3%;  Score 26.6;  DB 6;  Length 394191;
  Best Local Similarity   71.4%;  Pred. No. 50;
  Matches   35;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         28 CAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAA 76
              ||||  ||||||| |||||| |||| |||| |||| |     ||  |||
Db       4279 CAAGATCTTCATCTTACAAGATCATTCTGGCTGCAGAATGGAAAAGGAA 4231


RESULT 7
US-10-953-349-15193
; Sequence 15193, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15193
;   LENGTH: 1068
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15193

  Query Match             13.2%;  Score 26.4;  DB 6;  Length 1068;
  Best Local Similarity   47.0%;  Pred. No. 5;
  Matches   78;  Conservative    1;  Mismatches   87;  Indels    0;  Gaps    0;

Qy         10 TCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAG 69
              | || | |   || | |||||||||    |   |  ||  |   |  ||| |||   | |
Db        186 TTATGTCTCTGAGCTTCTCAAGGCACACTGGCGGCAGAGGAGTGGTGGCTGCGTCCTCAA 245

Qy         70 AAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCA 129
                ||  ||    |   |         |  | :|  ||||    || ||||  ||||   |
Db        246 CGGTAGACACAAACAATATGCCGATGACAGGAGTGGTGTTCCAGCCGTTCGAGGAGGTGA 305

Qy        130 CACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCAC 175
              ||||  ||| | ||| | | ||    |   |    ||| ||| |
Db        306 AGAAAGCCGATCTGGCCATTCCAATCACATCTAATGCCTCCCTCGC 351


RESULT 8
US-10-953-349-9738
; Sequence 9738, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9738
;   LENGTH: 3420
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9738

  Query Match             13.2%;  Score 26.4;  DB 6;  Length 3420;
  Best Local Similarity   54.3%;  Pred. No. 8.3;
  Matches   51;  Conservative    1;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         51 ATCCTGGGTGCACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCT 110
              ||   ||||   | | ||||| | || | | | | ||| |||  |  |||:|||   |

Db        770 ATATGGGGTTTTCTCGAAGAAATCAATCGCCAGTATCAGGTTTTGAGAATGGAAACTTGG 829

Qy        111 AGGCTGTTCTTGGAGCCCACACAAGCAGATATTG 144
                | || | ||    | |   | ||| ||  |||
Db        830 TAGATGGTTTTCAGCCACTTTCTAGCCGAACTTG 863


RESULT 9
US-10-511-937-2815/c
; Sequence 2815, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2815
;   LENGTH: 6050
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2815

  Query Match             13.2%;  Score 26.4;  DB 6;  Length 6050;
  Best Local Similarity   50.0%;  Pred. No. 11;
  Matches   66;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy          1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG 60
              |||  |||  |||  |||     |   ||     || |   | |    || ||||||| ||
Db        505 TTGCCATAGTCAATTTTGGACGTGACTTTCTGCTTCAGTTCCTTCAGCTCATCCTTGGGT 446

Qy         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
              |          || ||| || | | |||   | ||  | || | |     | | |||  |
Db        445 AAGGTTCCTGAGAGAAGCTGGGACCTCCACTCCATCAGATCGTACATCATGGACTGCACC 386

Qy        121 TGGAGCCCACAC 132
              |||||   || |
Db        385 TGGAGAAAACGC 374


RESULT 10
US-11-293-697-1913/c
; Sequence 1913, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1913
;   LENGTH: 3059
;   TYPE: DNA
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```
;   ORGANISM: Homo sapiens
US-11-293-697-1913

  Query Match             13.1%;  Score 26.2;  DB 7;  Length 3059;
  Best Local Similarity   51.3%;  Pred. No. 9.3;
  Matches   58;  Conservative    1;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         15 TTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTG 74
              ||||||  ||||||  | |   ||     |||   |   |   |  |||||  |
Db       2902 TTTTCTGTCTCCTCATTGTCAGAATAAATTAAGAGAAAAAGTGAAATTTAGGAAGAAAGG 2843

Qy         75 AACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
                ||     ||||   | | || |||:||   |||||  |  ||||||   |||
Db       2842 GGCCCGCTCTCTCCGATCCTGGTAATAGATAAGTCTATGTGGTTCTTCTGGCC 2790


RESULT 11
US-11-217-529-79011
; Sequence 79011, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79011
;   LENGTH: 1008
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79011

  Query Match             12.7%;  Score 25.4;  DB 7;  Length 1008;
  Best Local Similarity   53.5%;  Pred. No. 11;
  Matches   53;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         56 GGGTGCACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCT 115
              || ||||  |  | ||   |||  | |||           ||||  | |||||   ||
Db         75 GGATGCAGAAAACGAGTGGAATGTGGAAAAATTCAAAAAGGACTTCGAAGTCAATATTTC 134

Qy        116 GTTCTTGGAGCCCACACAAGCAGATATTGCCTTGCTAAA 154
              ||  || ||  | | | |  || || | | |||| ||||
Db        135 GTCATTAGACGCAAGAGAGACAAATTTCGACTTGATAAA 173


RESULT 12
US-11-217-529-76402/c
; Sequence 76402, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76402
;   LENGTH: 1734
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76402

  Query Match             12.6%;  Score 25.2;  DB 7;  Length 1734;
  Best Local Similarity   53.1%;  Pred. No. 16;
  Matches   51;  Conservative    1;  Mismatches   44;  Indels    0;  Gaps    0;

Qy         65 CCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGA 124
              ||||   || | | ||| ||  | | |||| || ||: |   ||  |  ||  | ||||
Db        940 CCAATCTGTAAGCTTCGTATTGCTTCTTCAAGACATGCATACGTTCATTCTTCTTTTGGG 881

Qy        125 GCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAG 160
                | ||  | | | |  ||  ||   |  || | ||
Db        880 CACGACCAACGTATAACTTTTCTCCATTTAGTTCAG 845


RESULT 13
US-11-293-697-740/c
; Sequence 740, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 740
;   LENGTH: 2638
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-740

  Query Match             12.6%;  Score 25.2;  DB 7;  Length 2638;
  Best Local Similarity   54.3%;  Pred. No. 19;
  Matches   51;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          7 TCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACC 66
              ||| | |   | |     |  || || |   |  |||| |||||   |||||  |||
Db       1751 TCCCCTTTCCTGCCCTCTTTTCCAGTCTGGCTGCCTAGAAGGTGGACCTGGTAGCAATGA 1692

Qy         67 AAGAAGTGAACCTCGAATCTCATGTTCAGGAAAT 100
                |  ||||||  |  |  |||||    |||| | |
Db       1691 GATCAGTGAATCCTGGGTCTCAATACCAGGGAGT 1658


RESULT 14
US-10-488-619-2493/c
; Sequence 2493, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Association
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2493
;   LENGTH: 631
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2493

  Query Match             12.5%;  Score 25;  DB 6;  Length 631;
  Best Local Similarity   50.4%;  Pred. No. 12;
```

Matches 58; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

```
Qy          81 GAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACACAAGCAGAT 140
               | | ||   |||| |  || :|  ||  |    ||||| |  |||||   | |  | |
Db         321 GGAGCTGGAGTTCTGTGAAAAGCTGTTACAGACCTGTTTCTCTAGCCCTACCGACGACAG 262

Qy         141 ATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTGGTCTTCACCCCACGC 195
                 ||  | ||| |  | | |  | | || |||  |      ||     |||||| ||
Db         261 CATGGATCGCTGAGACCAGGTGGCTCCTTGCTTTCTCTCCGTGGGAACCCCAGGC 207
```

RESULT 15
US-10-505-928-226
; Sequence 226, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 226
; LENGTH: 4908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-226

Query Match 12.5%; Score 25; DB 6; Length 4908;
Best Local Similarity 59.7%; Pred. No. 29;
Matches 40; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

```
Qy          88 ATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACACAAGCAGATATTGCCT 147
               || |  |  || |:|||   || ||| |  |||||||  |  ||||| | || |    |
Db        1079 ATCTAAACTAACTAGAATCCTCCAGGATTCTCTTGGAGGGCGTACAAGAACATCTATAAT 1138

Qy         148 TGCTAAA 154
               ||| | |
Db        1139 TGCAACA 1145
```

Search completed: May 26, 2006, 14:28:53
Job time : 25 secs